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g935.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2871>:

m935.seq

```

1 ATGTTGTATT TCAGATACGG CTTTTGGTT GTTGGTGTG CGGCAGGTGT
51 TTCTGCCGCC TATGGGGCGG ATGCGCCCGC GATTTGGAT GACAAGGCAT
101 TGTTGCAGGT GCAGCGGTG GTGTCGGATA AGTGGGCGGA ATCGGATTGG
151 AAAGTTGAAA ATGATGCCCG GCGCGTGGTT GACGGGGATT TTTGTTGGC
201 GCATCCGAAA ATGTTGAAAC ATAGTTGCG CGACCGCCTC AACGGCAATC
251 AGGCGGATTT AATCGCTTCG TTGGCGGATT TGTATGCCAA GCTGCCGGAT
301 TATGACCGCGG TTTGTAACGG CAGGGCGCGG GCTTGCTGG CGAAATTGGC
351 GGGAAAGGCCG GCGGAGGCCG TGGCGCGGTA TCGGGAACCTG CACGGGGAAA
401 ATGCGGCCAGA CGAGCGGATT TTGCTGGATT TGGCGCGGC GGAGTTTGAC
451 GATTTCCGGC TGAAGTCGGC AGAAAAGGCAT TTGCGGAGG CGGCAAAATT
501 GGATTTGCCG GCACCGGTT TGGAAAATGT GGGGGCGTTT CGGAAAAAAA
551 CGGAGGGCT GACGGGCTGG CGTTTTCGG GCGGCATCAG TCCGGCGGTG
601 AATAGAAATG CCAATAATGC CGCGCCGCAA TATTGCGGGC AAAACGGAGG
651 CCGGAGATA TGCAGTGTCA GCGGGCGGA GCGGGCGGC GGAGTTGAATT
701 ATGAAATCGA GGGCGAAAAG CTGACGCCGT TGGCAGATAA TCATTATTTG
751 TTGTTCCGTT CCAATATCGG CGGCACGAGC TATTATTTCA GTAAAAAAATC
801 AGCTTATGAT GACGGGTTCG GCAGGGCGTA TTTGGGTTGG CAGTATAAAA
851 ATGCACGGCA GACGGCGGGG ATTTTGCCT TTTATCAGGT GCAGTTGTCG
901 GGCAGCGACG GCTTGTGTC GAAAACAAAA CGGGTAAACA ACCGCGCCT
951 GCCGCGGTAT ATGCTGGCGC ACGGAGTCGG CGTGCAGCTG TCCCATACTT
1001 ACCGCCAAA CCCGGATGG CAATTTCGG TCGCGCTGGA ACATTACCGC
1051 CAAACGCTACC GCGAACAGGA TAGGGCGGA TACAATAACG GCAGGCAGGA
1101 CGGGTTTAT GTTCTGTCGG CAAAACGTTT GGGCGAATCG GCAACTGTGT
1151 TCGGCGCTG GCAGTTGTG CGGTTTGTG CGAAACGCGA AACGGTGGGC
1201 GCGCGGGTCA ATAATGCCGC CTACCGGGCGC AACGGTGGTT ATGCCGGTTG
1251 GCGCAGGAG TGGCGGCAGT TGGCGGGTT GAACAGTCGG GTTTCGGCGT
1301 CTTATGCCCG CCGCAACTAT AAGGGCATTG CGGCTTCTC GACAGAGGCG
1351 CAACGCAACC GCGAATGGAA TGTCTCGCTG GCTTGAGCC ACGACAAGTT
1401 GTCGTACAAA GGTATCGTGC CGCGCTTGAA TTATCGTTT GGCAGGACGG
1451 AAAGTAATGT GCGTATGCG AAACGCGCA ACAGCGAGGT GTTGTGTCG
1501 GCGGATTGGC GGTTTGAA

```

This corresponds to the amino acid sequence <SEQ ID 2872; ORF 935>:

m935.pep

```

1 MLYFRYGFV VVCAAGVSAA YGADAPAILD DKALLQVQRS VSDKWAESDW
51 KVENDAPRVV DGDFLLAHPK MLEHSLRDAL NGNQADLIAS LADLYAKLPD
101 YDAVLYGRAR ALLAKLAGRP AEAVARYREL HGENAADERI LLDLAAAEDF
151 DFLRLKSAERH FAEAAKLDLP APVLENVGRF RKKTEGLTW RFSGGISPAV
201 NRNANNAAPQ YCRQNNGRQI CSVSRAERAA GLNYEIEAEK LTPLADNHYL
251 LFRSNIGGTS YYFSKKSAYD DGFGRAYLGW QYKNARQTAG ILPFYQVQLS
301 GSDGFDATK RVNNNRLPPY MLAHGVGVQL SHTYRPNPWG QFSVALEHYR
351 QRYREQDRAE YNNQRQDGFY VSSAKRLGES ATVFGGWQFV RFVPKRETVG
401 GAVNNAAYRR NGVYAGWAQE WRQLGGLNSR VSASYARRNY KGIAAFSTEA
451 QRNREWNVSL ALSHDKLSYK GIVPALNYRF GRTESNVPYA KRRNSEVFVS
501 ADWRF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2873>:

a935.seq

```

1 ATGTTGTATT TCAGATACGG TTTTTGGTT GTTGGTGTG CGGCAGGTGT
51 TTCTGCCGCC TATGGGGCGG ATGCGCCCGC GATTTGGAT GACAAGGCAT
101 TGTTGCAGGT GCAGCGGTG GTGTCGGATA AGTGGGCGGA ATCGGATTGG
151 AAAGTTGACA ATGATGCCCG GCGCGTGGTT GACGGGGATT TTTGTTGGC
201 GCATCCGAAA ATGTTGAAAC ATAGTTGCG CGACGTGCTC AACGGCAATC
251 AGGCGGATTT GATCGCTTCG TTGGCGGATT TGTATGCCAA GCTGCCGGAT
301 TATGACCGGG TTTGTAACGG CAGGGCGCGG GCTTGTGCTGG CGAAATTGGC
351 GGGAAAGGCCG CGGGAGGCCG TGGCGCGGTA TCGGGAACCTG CACGGGGAAA
401 ATGCGGCCAGA CGAGCGGATT TTGCTGGATT TGGCGCGGC GGAGTTTGAC
451 GATTTCCGGC TGAAGTCGGC AGAAAAGGCAT TTGCGGAGG CGGAAAAATT
501 GGATTGCGG CGCGCCGGTT TGGAAAATGT GGGGGCGTTT CGGAAAAAG
551 CGGAGGGGCT GACGGGCTGG CGTTTTCGG GCGGCATCAG TCCGGCGGTG

```

1350

	310	320	330	340	350	360
m935.pep	GSDGFDAKTKRVNNNRLPPYMLAHGVGVQLSHTYRPNPQWQFSVALEHYRQRYREQDRAE					
a935	GSDGFDAKTKRVNNNRLPPYMLAHGVGVQLSHTYRPNPQWQFSVALEHYRQRYREQDRAE					
	310	320	330	340	350	360
m935.pep	370	380	390	400	410	420
a935	YNNGRQDGFYVSSAKRLGESATVFGGWQFVRFVPKRETVGGAVNNAAYRRNGVYAGWAQE					
	370	380	390	400	410	420
m935.pep	WRQLGGLNSRVSASYARRNYKGIAAFSTEAQRNREWNVSLALSHDKLSYKGIVPALNYRF					
a935	WRQLGGLNSRVSASYARRNYKGVAAFSTEAQRNREWNVSLALSHDKLSYKGIVPALNYRF					
	430	440	450	460	470	480
m935.pep	GRTESNVPYAKRRNSEVFVSADWRFX					
a935	GRTESNVPYAKRRNSEVFVSADWRFX					
	490	500				
m935.pep	490	500				
a935	490	500				

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2875>:

g936.seq

```

1 ATGAAACCCA AACCGCACAC CGTCCGCACC CTGATTGCCG CCGTCCTCAG
51 CCTTGCCCTC GGCGGCTGCT TCAGCGCAGT CGTCGGCGGG GCCGCCGTG
101 GCGCAAAATC CGTCATCGAC CGccgAACCA CCGgcgcgc AACCGATGac
151 aACGTTATGG CGTTGCGTAT CGAAACCACC GCCCCTTCT ACCTGCGCCA
201 AAACAACCAA ACCAAAGGCT ACACGCCCA AATCTCCGTC GTCCGGCTACA
251 ACCGCCACCT GCTGCTGCTC GGACAAGTCG CCACCGAAGG CGAAAAACAG
301 TTCGTCGGTC AGATTGCACG TTCCGAACAG GCCGCCGAAG GCGTATAACAA
351 CTACATTACC GTCGCCTCCC TGCCGCGCAC TGCGGGCGAC ATCGCCGGCG
401 ACACTTGGAA CACGTCCAAA GTCCGCGCca cgCTGCTGGG CATCAGCCCC
451 GCTACACAGG CGCGCGTCAA AATCATTACC TACGGCAATG TAACCTACGT
501 TATGGGCATC CTCACCCCCG AAGAACAGGC GCAGATTACC CAAAAAGTCA
551 GCACCAccgT CGCGTACAA AAAGTCATTA CCCTCTACCA AAAACTACGTC
601 CAACGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2876; ORF 936.ng>:

g936.pep

```

1 MKPKPHTVRT LIAAVLSLAL GGCFSAVVG AAVGAKSVID RRTTGAQTDD
51 NVMALRIETT ARSYLRQNNO TKGYTPQISV VGYNRHLLL GQVATEGEKQ
101 FVGQIARSEQ AAEGVYNYIT VASLPRTAGD IAGDTWNTSK VRATLLGISP
151 ATQARVKIIT YGNVTYVMGI LTPEEQAQIT QKVSTTVGVQ KVITLYQNYV
201 QR*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2877>:

m936.seq (partial)

```

1 ATGAAACCCA AACCGCACAC CGTCCGCACC CTGATTGCCG CCATTTTCAG
51 CCTTGCCCTT AGCGGCTGCG TCAGCGCAGT AATCGGAAGC GCCGCCGTG
101 GCGCGAAATC CGCCGTCGAC CGCCGAACCA CCGGCGCGCA AACCGACGAC
151 AACGTTATGG CGTTGCGTAT CGAAACCACC GCCCCTTCT ATCTGCGCCA
201 AAACAACCAA ACCAAAGGCT ACACGCCCA AATCTCCGTC GTCCGGCTACA
251 ACCGCCACCT GCTGCTGCTC GGACAAGTCG CCACCGAAGG CGAAAAACAG
301 TTCGTCGGTC AGATTGCACG TTCCGAACAG GCCGCCGAAG GCCTGTACAA
351 CTATATTACC GTCGCCTCCC TGCCGCGCAC TGCC...

```

This corresponds to the amino acid sequence <SEQ ID 2878; ORF 936>:

m936.pep (partial)

```

1 MKPKPHTVRT LIAAIIFSLAL SGCVSAVIGS AAVGAKSAVD RRTTGAQTDD
51 NVMALRIETT ARSYLRQNNO TKGYTPQISV VGYNRHLLL GQVATEGEKQ
101 FVGQIARSEQ AAEGVYNYIT VASLPRTA...

```


a936 |||||||
 VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIVTYGNVTYVMGILTPEEQAQIT
 130 140 150 160 170 180

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2881>:
g936-1.seq

```

1 ATGAAACCCA AACACACAC CGTCCGCACC CTGATTGCCG CGCTCCTCAG
51 CCTTGCCCTC GGCGGTGCT TCAGCGCAGT CGTCGGCGGG GCGCCGCTCG
101 GCGCAAATC CGTCATCGAC CGccgAACCA CGGcgcgca AACCGATGac
151 aACGTTATGG CGTTGCGTAT CGAAACCAC CGCCGTTCT ACCTGCGCCA
201 AAACAACCAA ACCAAAGGCT ACACGCCCA AATCTCCGTC GTGGCTACA
251 ACCGCCACCT GCTGCTGCTC GGACAAGTCG CCACCGAAGG CGAAAAACAG
301 TTCTGTCGGTC AGATTGCAAG TTCCGAACAG GCCGCCGAAG GCGTATAACAA
351 CTACATTACCG TGCGCCTCC TGCGGCCAC TGCGGGCGAC ATCGCCGGCG
401 ACACTTGGAA CACGTCAAA CGCCGCTCAA cgCTGCTGGG CATCAGCCCC
451 CCTACACAGG CGCCGCTCAA AATCATTACCG TACGGCAATG TAACCTACGT
501 TATGGGCATC CTCACCCCCG AAGAACAGGC GCAGATTACCG CAAAAAGTCA
551 GCACCAAccgt CGGCGTACAA AAAGTCATTA CCCTCTACCA AAACATACGTC
601 CAACGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2882; ORF 936-1.ng>:
g936-1.pep

```

1 MKPKPHTVRL LIAAVLSLAL GGCFSAVVGG AAVGAKSVID RRTTGAQTDD
51 NVMALRIETT ARSYLRQNNO TKGYTPQISV VGYNRHLLLL GQVATEGEKQ
101 FVGQIARSEQ AAEGVNYIT VASLPRTAGD IAGDTWNTSK VRATLLGISP
151 ATQARVKIIT YGNVTYVMGI LTPEEQAQIT QKVSTTVGVQ KVITLYQNYV
201 QR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2883>:
m936-1.seq

```

1 ATGAAACCCA AACCGCACAC CGTCCGCACC CTGATTGCCG CCATTTTCAG
51 CCTTGCCCTC AGCGGTGCTC TCAGCGCAGT AATCGGAAGC GCGCCGCTCG
101 GCGCAAATC CGCCGCTCGAC CGCCGAACCA CGGCCGCGCA AACCGACGAC
151 AACGTTATGG CGTTGCGTAT CGAAACCAC CGCCGTTCTC ATCTGCGCCA
201 AAACAACCAA ACCAAAGGCT ACACGCCCA AATCTCCGTC GTGGCTACA
251 ACCGCCACCT GCTGCTGCTC GGACAAGTCG CCACCGAAGG CGAAAAACAG
301 TTCTGTCGGTC AGATTGCAAG TTCCGAACAG GCCGCCGAAG GCGTGTACAA
351 CTATATTACCG TGCGCCTCC TGCGCGCAC TGCGGGCGAC ATCGCCGGCG
401 ACACTTGGAA CACATCCAAA GTCCCGGCCA CGCTGTTGGG CATCAGCCCC
451 GCCCACACAGG CGCCGCTCAA AATCGTTACCG TACGGCAACCG TAACCTACGT
501 TATGGGCATC CTCACCCCCG AAGAACAGGC GCAGATTACCG CAAAAAGTCA
551 GCACCAAccgt CGGCGTACAA AAAGTCATCA CCCTCTACCA AAACATACGTC
601 CAACGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2884; ORF 936-1>:
m936-1.pep

```

1 MKPKPHTVRL LIAAIFSLAL SGCVSAIGS AAVGAKSAVD RRTTGAQTDD
51 NVMALRIETT ARSYLRQNNO TKGYTPQISV VGYNRHLLLL GQVATEGEKQ
101 FVGQIARSEQ AAEGVNYIT VASLPRTAGD IAGDTWNTSK VRATLLGISP
151 ATQARVKIIT YGNVTYVMGI LTPEEQAQIT QKVSTTVGVQ KVITLYQNYV
201 QR*

```

m936-1/g936-1 95.5% identity in 202 aa overlap

	10	20	30	40	50	60	
m936-1.pep	MKPKPHTVRL LIAAIFSLAL SGCVSAIGS AAVGAKSAVD RRTTGAQTDD NVMALRIETT	: : : : : : : : : : :	: : : : : : : : : : : :	: : : : : : : : : : : :	: : : : : : : : : : : :	: : : : : : : : : : : :	
g936-1	MKPKPHTVRL LIAAVLSLAL GGCGFSAVVGG AAVGAKSVID RRTTGAQTDD NVMALRIETT	10	20	30	40	50	60
	70	80	90	100	110	120	
m936-1.pep	ARSYLRQNQTKGYTPQISVVGYNRHLLLLGQVATEGEKQFVGQIARSEQAAEGVNYIT	: : : : : : : : : : : :	: : : : : : : : : : : :	: : : : : : : : : : : :	: : : : : : : : : : : :	: : : : : : : : : : : :	
g936-1	ARSYLRQNQTKGYTPQISVVGYNRHLLLLGQVATEGEKQFVGQIARSEQAAEGVNYIT	70	80	90	100	110	120
	130	140	150	160	170	180	
m936-1.pep	VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIVTYGNVTYVMGILTPEEQAQIT	: : : : : : : : : : : :	: : : : : : : : : : : :	: : : : : : : : : : : :	: : : : : : : : : : : :	: : : : : : : : : : : :	

g936-1	VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIITYGNVTYVMGILTPEEQAQIT
	130 140 150 160 170 180
	190 200
m936-1.pep	QKVSTTVGVQKVITLYQNYVQRX
g936-1	QKVSTTVGVQKVITLYQNYVQRX
	190 200

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2885>:
a936-1.seq

```

1 ATGAAACCCA AACCGCACAC CGTCCGCACC CTGACTGCCG CCGCCTCAG
51 CCTGCCCTC GGCGCTGCG TCAGCGAGT CGTCGGCGGC GCGCGGTGCG
101 CGCGAAATC CGCGCTGCAC CGCGAACCA CGCGCGCGCA AACCGACGAC
151 AACGTAATGG CGCTCGTAT CGAAACCACC CGCCGCTCCT ATCTGCGCCA
201 AAACAACCAA ACCAAGGCT ACACGCCCA AATCTCCGTT GTCGGCTACA
251 ACCGCCACCT GCTGCTGCTC GGACAAGTCG CCACCGAAGG CGAGAACAG
301 TTCGTCGGTC AGATTGACAG TTCCGAACAG GCGCGCGAAG GCGTGTACAA
351 CTACATTACC GTCGCTCCC TGCGCGCGAC TGCGCGCGAC ATCGCCGGCG
401 ACACTTGGAA CACATCCAAA GTCCGCGCCA CGCTGTTGGG CATCAGCCCC
451 GCCACACAGG CGCGCTCAA AATCGTTACC TACGGCAACG TAACCTACGT
501 TATGGGCATC CTCACCCCG AAGAACAGGC GCAGATTACC CAAAAAGTCA
551 GCACCACCGT CGCGTACAA AAAGTCATCA CCCTCTACCA AACTACGTC
601 CAACGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2886; ORF 936-1.a>:

a936-1.pep

```

1 MKPKPHTVRT LTAALVSLAL GGCVSAVVGG AAVGAKSAVD RRTTGAQTD
51 NVMALRIETT ARSYLRQQNNO TKGYTPQISV VGYNRHLLL GQVATEGEKQ
101 FVGQIARSEQ AAEGVYNYIT VASLFRTAGD IAGDTWNTSK VRATLLGISP
151 ATQARVKIVT YGNVTYVMGI LTPEEEQAQIT QKVSTTVGVQ KVITLYQNYV
201 QR*

```

a936-1/m936-1 97.0% identity in 202 aa overlap

m936-1.pep	10 20 30 40 50 60
	MKPKPHTVRTLIAAIFSLALSGCVSAVIGSAAVGAKSAVDRRTGAQTDNNVMALRIETT
a936-1	10 20 30 40 50 60
	: : : : : : : : : : : :
m936-1.pep	70 80 90 100 110 120
	ARSYLRQQNQTKGYTPQISVVGYNRHLLL GQVATEGEKQFVGQIARSEQAAEGVYNYIT
a936-1	70 80 90 100 110 120
	: : : : : : : : : : : :
m936-1.pep	130 140 150 160 170 180
	VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIVTYGNVTYVMGILTPEEQAQIT
a936-1	130 140 150 160 170 180
	: : : : : : : : : : : :
m936-1.pep	190 200
	QKVSTTVGVQKVITLYQNYVQRX
a936-1	190 200

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2887>:
g937.seq

```

1 atGAAAAATA TTCTCTTAgT ATTTGTTAGC TTTGTGCCAT TATGTGTCCG
51 CACTGATCTG CCGCTGAata tCGAAGACAT AATGaccgAC AAGGGAAAAT
101 GGAAactGGA AACTTccctt acctacctgA acaGCGAAAA cagCCGCGCC
151 GCACTTGCTC CACCGGTTTA CATTCAAGACCG GGCTCCGCTT CCTTTATCCC
201 CGTCCCGACC GAAATTCAAGG AAAACGGCAG CAATACCGAT ATGCTCGCCG
251 GCACGCTCGG TTTGCGCTAC GGACTGAccg GCAataccgA CATTACCGC
301 AGCGGCAGCT ATCTGTGGCA CGAAGAACGCG AAAACTCGacg GCAACGGCAA

```

351 AACCCGCAAC AAACGGATGT CCGACATATC CGCCGGCATC AGCCACACCT
 401 TCCttaAAGa cgGCAAAAT CCCGCACTCA TCGCTTCCCT CGAAAGCACG
 451 GTTTACGAAA AATCGCGCAA CAAAGCCTCG TCAGGAAAAT CGTGGCTCAT
 501 CGGCGCCACC ACCTACAAAG CCATAGATCC GATTGTCCTT TCCCTCACCG
 551 CGGCCTACCG CATCAACGGC AGCAAAACCC TTTCAGACGA CGTCAAATAC
 601 AAACCGAGCA ATTACTGGAT GCTGAATCCC AACATCTCAT TTGCCGCCAA
 651 CGACAGAACATC AGCCTGACCG GAGGCATCCA ATGGCTGGGC AAACAGCCCG
 701 ACCGCATAGA CGGCAAAAAA GAATCCGCAA GAAACACATC CACCTACGCC
 751 CATTTCGGCG CAGGTTTCGG TTTCACCAAA ACCGGGCTT TAAACGCATC
 801 CGCACGTTTC AACGTTTCAG GGCAAAGCAG TTCCGAAC TG AAATTGGCG
 851 TACAGCATAAC ATTTTAA

This corresponds to the amino acid sequence <SEQ ID 2888; ORF 937.ng>
 g937.pep

1 MKNILLVFS FVPLCVRTDL PLNIEDIMTD KGKWKLETS TYLSENSRA
 51 ALASPVYIQT GSASFIPVPT EIQQENGNTD MLAGTLGLRY GLTGNTDIY
 101 SGSYLWHEER KLDGNGKTRN KRMSDISAGI SHTFLKDGN PALIAFLEST
 151 VYEKSRNKAS SGKSWLIGAT TYKAIDPIVL SLTAAYRING SKTLSDDVKY
 201 KAGNYWMLNP NISFAANDRI SLTGGIQWLQ KQPDRIDGKK ESARNTSTYA
 251 HFGAGFGFTK TAALNASARF NVSGQSSSEL KLGVQHTF*

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2889>:
 m937.seq

1 ATGAAGCGCA TCTTTTGCC CGCCTTGCCC GCCATCCTGC CTTTATCCAC
 51 TTATGCCGAC CTGCCCTTGA CGATTGAAGA CATAATGACC GACAAGGGAA
 101 AATGGAAACT GGAAACTTCC CTTACCTTAC TGAACAGCGA AAACAACCGC
 151 GCCGAACCTTG CGCACCGGT TTACATTCAA ACCGCGCAA CCTCGTTTAT
 201 CCCCATTCCG ACCGAAATCC AAgAAAaCGG CAGCAATACC GATATGCTCG
 251 TCGGCACGCT CGGTTTGCAC TACGGACTGA CCGGAAATAC CGACATTAC
 301 GGCAGCGGCA GCTATCTGT GCACGAAGAA CGCAAACCTCG ACGGCAACAG
 351 CAAACCCGC AACAAACGGA TGTCCGACGT ATCCCTCGGC ATCAGCCACA
 401 CTTTCCTTAA AGACGACAAA AACCCCGCCC TAATCAGCTT TCTTGAAAGC
 451 ACGGTTTACG AAAATCGCG CAACAAAGCC TCGTCGGGAA AATCTGGCT
 501 CATCGGGCC ACCACCTACA AAGCCATAGA TCCGATTGTC CTTTCCCTCA
 551 CCGCCGCCTA CGCATCAAC GGCAGCAAAA CCCTTCAGA CGGCATCCGC
 601 TACAAATCGG GCAACTACCT GCTGCTCAAC CCCAACATCT CATTGCTGC
 651 CAACGACAGA ATCAGCCTGA CCGGAGGCAT CCAATGGCTG GGCAGGCAGC
 701 CCGACCGGAC GGACGGCAAA CGGGAATCCT CCAGAAACAC ATCCACCTAC
 751 GCCCATTCTG GCGCAGGTTT CGGTTTCAACC AAAACACCGG CTTTAAACGC
 801 ATCCGCACGT TTCACGTTT CAGGGCAAAG CAGTCCGAA CTGAAATTG
 851 GCGTACAGCA TACATTTAA

This corresponds to the amino acid sequence <SEQ ID 2890; ORF 937>:
 m937.pep..

1 MKRIFLPALP AILPLSTYAD LPLTIEDIMT DKGKWKLETS LTYLSENNR
 51 AELAAPVYIQT TGATSFIPVPT TEIQENGNTD DMLVGLGLRY YGLTGNTDIY
 101 GSGSYLWHEER RKLDGNSKTRN KRMSDISVSLG ISHTFLKDDK NPALISFLES
 151 VYEKSRNKAS SSGKSWLIGA TTYKAIDPIV LSLTAAYRIN GSKTLSDGIR
 201 YKSGNYLLN PNISFAANDR ISLTGGIQWLQ GRQPDRTDGK RESSRNTSTYA
 251 AHFGAGFGFTK TTALNASARF FNVSGQSSSE LKFGVQHTF*

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N.gonorrhoeae*

ORF 937 shows 86.9% identity over a 289 aa overlap with a predicted ORF (ORF 937.ng)
 from *N.gonorrhoeae*:

g937/m937

g937.pep	10 20 30 40 50 59
	MKNILL-VFVSFVPLCVRTDLPLNIEDIMTDKGKWKLETSLYLSENNRAALASPVYIQT
m937	: :: : ; : : : : : : : :
	MKRIFLPALPAILPLSTYADLPLTIEDIMTDKGKWKLETSLYLSENNRAELAAPVYIQT
	10 20 30 40 50 60
g937.pep	60 70 80 90 100 110 119
	TGSASFIPVPTEIQENGNTDMLAGTLGLRYGLTGNTDIYGSGSYLYWHEERKLDGNGKTR

m937	TGATSFIPIPTEIQENGNSNTDMLVGTGLRYGLTGNTDIYGSGSYLWHEERKLDGNSKTR						
	70	80	90	100	110	120	
g937.pep	120	130	140	150	160	170	179
	NKRMMSDISAGISHTFLKDGPALIAFLESTVYEKSRNKASSGKSWLIGATTYKAIDPIV						
m937	NKRMMSDVSLGISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGATTYKAIDPIV						
	130	140	150	160	170	180	
g937.pep	180	190	200	210	220	230	239
	LSLTAAAYRINGSKTLSDDVKYKAGNYWMNPNISFAANDRISLTGGIOWLKGQPDRIDGK						
m937	LSLTAAAYRINGSKTLSDGIRYKSGNYLLLNPNISFAANDRISLTGGIOWLGRQPDRTDGK						
	190	200	210	220	230	240	
g937.pep	240	250	260	270	280	289	
	KESARNTSTYAHFGAGFGFTKTAALNASARFNVSGQSSSELKLGVQHTFX						
m937	RESSRNTSTYAHFGAGFGFTKTTALNASARFNVSGQSSSELKFGVQHTFX						
	250	260	270	280			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2891>:

a937.seq

1	ATGAAGCGCA	TCTTTTGCC	CGCCTTGC	GCCATCCTGC	CTTTATCCGC	
51	TTATGCCGAC	CTGCCCTG	CGATTGAAGA	CATAATGACC	GACAAGGGCA	
101	AATGGAAACT	GGAAACTTCC	CTTACCTACC	TGAACAGCGA	AAACAACCGC	
151	GCCGAACCTG	CCGCACCGGT	TTACATCCAA	ACCGGCGAA	CCTCGTTAT	
201	CCCCATTCCG	ACCGAAATCC	AAGAAAACGG	CAGCAATACC	GATATGCTCG	
251	TTGGCACGCT	CGGTTTGC	TACCGACTGA	CCGGGAATAC	CGACATTTAC	
301	GGCAGCGGCA	GCTATCTGTG	GCACGAAGAA	CGCAAACCTCG	ACGGCAACCGG	
351	CAAAACCGA	AACAAACCGA	TGTCCGACGT	ATCCCTCGGC	ATCAGCCACA	
401	CCTTCCTTAA	AGACGACAAA	AACCCCGCCC	TAATCAGCTT	TCTTGAAAGC	
451	ACGGTTTACG	AAAAATCGCG	CAACAAAGCC	TCGTCGGAA	AATCTGGCT	
501	CATCGGCGCC	ACCACCTACA	AAGCCATCGA	CCCCGTCGTC	CTCTCATTA	
551	CCGCTGCCTA	CCGTATCAAC	GGCAGCAAA	CCCTTTCAAG	CAACACCAAA	
601	TACAAAGCAG	GCAATTACTG	GATGCTGAAT	CCCAATATAT	CCTTCGCCGC	
651	CAACGACAGA	ATCAGCCTCA	CGGGCGGCAT	CCAATGGCTG	GGCAAGCAGC	
701	CCGACCGTCT	GGACGGCAAA	AAAGAATCCG	CAAGAAACAC	ATCCACCTAT	
751	GCCCATTTCG	GCGCAGGTTT	CGGTTTCACC	AAAACCACGG	CTTTAAACGC	
801	ATCCGCACGT	TTCAACGTTT	CAGGGCAAAG	CAGTTCCGAA	CTGAAATTG	
851	CGTACAGCA	TACGTTTAA				

This corresponds to the amino acid sequence <SEQ ID 2892; ORF 937.a>:

a937.pep

1	MKRIFLPALP	AILPLSAYAD	LPLTIEDIMT	DKGKWKLETS	LTYLSENNR	
51	AELAAPVYIQ	TGATSFIPIP	TEIQENGNSNT	DMLVGTGLR	YGLTGNTDIY	
101	GSGSYLWHEE	RKLDGNGKTR	NKRMMSDVSLG	ISHTFLKDDK	NPALISFLES	
151	TVYEKSRNKA	SSGKSWLIGA	TTYKAIDPVV	LSLTAAYRIN	GSKTLSSNTK	
201	YKAGNYWMN	PNISFAANDR	ISLTGGIOWL	GKQPDRLDGK	KESARNTSTY	
251	AHFGAGFGFT	KTTALNASAR	FNVSGQSSSE	LKFGVQHT*		

m937/a937 95.2% identity in 289 aa overlap

m937.pep	10	20	30	40	50	60
	MKRIFLPALPAILPLSTYADLPLTIEDIMTDKGKWKLETSLYLSENNRAELAAPVYIQ					
a937	MKRIFLPALPAILPLSAYADLPLTIEDIMTDKGKWKLETSLYLSENNRAELAAPVYIQ					
	10	20	30	40	50	60
m937.pep	70	80	90	100	110	120
	TGATSFIPIPTEIQENGNSNTDMLVGTGLRGLTGNTDIYGSGSYLWHEERKLDGNSKTR					
a937	TGATSFIPIPTEIQENGNSNTDMLVGTGLRGLTGNTDIYGSGSYLWHEERKLDGNGKTR					
	70	80	90	100	110	120

m937.pep	130	140	150	160	170	180
	NKRMSDVS LGISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGATTYKAIDPIV					
a937						
	NKRMSDVS LGISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGATTYKAIDPVV					
m937.pep	130	140	150	160	170	180
	LSLTAA YRINGSKTLSDGIRYKSGNYLLLNPNSFAANDRISLTGGI QWLGRQPDRDGK					
a937	: : :					
	LSLTAA YRINGSKTLSSNTKYKAGNYWMLNPNSFAANDRISLTGGI QWLKGQPDRLDGK					
m937.pep	190	200	210	220	230	240
	RESSRN TSTYAHFGAGFGFTKTTALNASARFN VSGQSS SELKFGVQHTFX					
a937	: :					
	KESARN TSTYAHFGAGFGFTKTTALNASARFN VSGQSS SELKFGVQHTFX					
m937.pep	250	260	270	280	290	
	250 260 270 280 290					
a937	250 260 270 280 290					

g939.seq not found yet

g939.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2893>:
 m939.seq (partial)

```

 1 ATGAAACGAT TGACTTTATT GCCCTTGTT TTGGCTGCCG GTGC GGTTTC
 51 CGCCTCTCCC AAAGCAGACG TGGAAAAGG CAAACAGGTT GCCGCAACCG
101 TTTGTGCGGC TTGCATGCA GCAGACGGTA ACAGCGGCAT TCGGATGTAT
151 CGCGTTTGG CGGCACAGCA TACTGCTTAC ATCTATCATC AACTATCGG
201 CATCCCGCAC GTAAACGCAC CC...
  
```

This corresponds to the amino acid sequence <SEQ ID 2894; ORF 939>:

m939.pep (partial)

```

 1 MKRLTLLAFV LAAGAVSASP KADVEKGKQV AATVCAACHA ADGN SGIA MY
 51 PRLAAQHTAY IYHQTIGIRD VNAP...
  
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2895>:
 a939.seq

```

 1 ATGAAACGAT TGACTTTATT GCCCTTGTT TTGGCTGCCG GTGC GGTTTC
 51 CGCATCTCCC AAAGCAGACG TGGAAAAGG CAAACAGGTT GCCGCAACCG
101 TTTGTGCGGC TTGCATGCA GCAGACGGTA ACAGCGGCAT TCGGATGTAT
151 CGCGTTTGG CGGCACAGCA TACTGCTTAC ATCTATCATC AACC ATCGG
201 CATCCCGCAC GGTAAACGCA CCCACGGTTC GGCAGCTGTG ATGAAACGG
251 TGGTAATGAA TTTGAGCGAT CAGGATATT TGAAACGTATC CGCATTCTAT
301 GCCAACACAGC AGCCAAATC CGGTGAAGCC AATCCTAAGG AAAATCCCGA
351 ATTGGGTGCG AAAATCTATC GCGGC GGTTT GAGCGATAAAA AAAGTGC CGG
401 CGTGTATGTC CTGCCACGGT CCGAGCGGTG CGGGTATGCC GGGGGCGG
451 AGCGAAATTC AGGCTTATCC GCGTTTGGGC GGT CAGCATC AGGCATATAT
501 TGTGAACAG ATGAATGCCT ACAAGTCCGG TCAGCGTAAA AATACCATCA
551 TGGAAAGATAT TGCAAACCGT ATGTC TGAAG AAGATTGAA AGCGGTGCC
601 AACTTATCC AAGGTTGCG TTAA
  
```

This corresponds to the amino acid sequence <SEQ ID 2896; ORF 939.a>:

a939.pep

```

 1 MKRLTLLAFV LAAGAVSASP KADVEKGKQV AATVCAACHA ADGN SGIA MY
 51 PRLAAQHTAY IYHQTIGIRD GKRTHGSAAV MKPVVMNLSD QDILNVSAFY
101 AKQQPKSGEA NPKENPELGA KIYRGGLSDK KVPACMSCHG PSGAGMPGGG
151 SEIQAYPRLG GQHQAYIVEQ MNAYKSGQRK NTIMEDIANR MSEEDLKAVA
201 NFIQGLR*
  
```

m939/a939 100.0% identity in 70 aa overlap

m939.pep	10	20	30	40	50	60
	MKRLTLLAFVLAAGAVSASP KADVEKGKQVAATVCAACHA ADGN SGIA MY PRLAAQHTAY					
a939						
	MKRLTLLAFVLAAGAVSASP KADVEKGKQVAATVCAACHA ADGN SGIA MY PRLAAQHTAY					

10 20 30 40 50 60

70

m939.pep	IYHQTIGIRDVNAP
a939	IYHQTIGIRDGKRTHGSAAVMKPVVMNLSDQDILNVSAYKQQPKSGEANPKENPELGA
	70 80 90 100 110 120

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2897>:

m950.seq

```

1 ATGAACAAAAA ATATTGCTGC CGCACTCGCC GGTGCTTTAT CCCTGTCTCT
51 GGCCGCCGGC GCCGTTGCGG CCCACAAACC GGCAAGCAAC GCAACAGGGCG
101 TTCAAAAATC CGCCCAAGGC TCTTGCGGCG CATCCAAATC TGCCGAAGGT
151 TCGTGCGGCG CATCCAAATC TGCCGAAGGT TGCTGCAGGG CGGCTGCTTC
201 TAAAGCAGGC GAAGGCAAAT GCAGGCGAGGG CAATGCGGT GCAACTGTAA
251 AAAAACCCCA CAAACACACC AAAGCATCTA AAAGCAAAGC CAAATCTGCC
301 GAAGGCAAAT GCGGCGAAGG CAAATGCGGT TCTAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2898; ORF 950.ng>:

m950.pep

```

1 MNKNIAAALA GALSLSLAAG AVAAHKPASN ATGVQKSAQG SCGASKSAEG
51 SCGASKSAEG SCGAAASKAG EGKCGEGKCG ATVKKAHKHT KASKAKAKSA
101 EGKCGEGKCG SK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2899>:

m950.seq

```

1 ATGAACAAAAA ACATTGCTGC CGCTCTCGCC GGTGCTTTAT CCCTGTCTTT
51 GGCCGCCGGT GCAGTTGCTG CCAACAAACC GGCAAGCAAC GCAACAGGGCG
101 TTCAAAATC CGCCCATGGC TCTTGCAGGG CGTCCAAATC TGCCGAAGGT
151 TCGTGCAGGG CGGCTGGTTC TAAAGCAGGC GAAGGCAAAT GCAGGCGAGGG
201 CAAATGCGGT GCGACCGTAA AAAAACCCCA CAAACACACC AAAGCATCTA
251 AAGCCAAGGC CAAATCTGCC GAAGGCAAAT GCGGCGAAGG CAAATGCGGT
301 TCTAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2900; ORF 950>:

m950.pep

```

1 MNKNIAAALA GALSLSLAAG AVAAANKPASN ATGVHKSAG SCGASKSAEG
51 SCGAAASKAG EGKCGEGKCG ATVKKTHKHT KASKAKAKSA EGKCGEGKCG
101 SK

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 950 shows 86.6% identity over a 112 aa overlap with a predicted ORF (ORF 950) from *N. gonorrhoeae*

m950/g950 86.6% identity in 112 aa overlap

m950.pep	10	20	30	40	50	

g950						-----
	10	20	30	40	50	60
m950.pep	60	70	80	90	100	
	---	AGSKAGEGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSK				-----
g950	70	80	90	100	110	
	SCGAAASKAGEGKCGEGKCGATVKKAHKHTKASKAKAKSAEGKCGEGKCGSKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2901>:

a950.seq

```

1 ATGAACAAAAA ACATTGCTGC CGCACTCGCC GGTGCTTTAT CCCTGTCTTT
51 GGCCGCCGGT GCAGTTGCTG CCAACAAACC GGCAAGCAAC GCAACAGGGCG
101 TTCAAAATC CGCCCATGGC TCTTGCAGGG CGTCCAAATC TGCCGAAGGT
151 TCGTGCAGGG CGGCTGGTTC TAAAGCAGGC GAAGGCAAAT GCAGGCGAGGG
201 CAAATGCGGT GCGACCGTAA AAAAACCCCA CAAACACACC AAAGCATCTA
251 AAGCCAAGGC CAAATCTGCC GAAGGCAAAT GCGGCGAAGG CAAATGCGGT
301 TCTAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2902; ORF 950.a>:
a950.pep

```

1 MNKNIAALALA GALSLSLAAG AVAANKPASN ATGVHKSAGH SCGASKSAEG
51 SCGAAGSKAG EGKCGEGKCG ATVKKTHKHT KASKAKAKSA EGKCGEGKCG
101 SK*

```

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. meningitidis*

ORF 950 shows 100.0% identity over a 102 aa overlap with a predicted ORF (ORF 950) from *N. meningitidis*

a950/m950 100.0% identity in 102 aa overlap

	10	20	30	40	50	60
a950.pep	MNKNIAALALA	GALSLSLAAG	AVAANKPASN	ATGVHKSAGH	SCGASKSAEG	
m950	MNKNIAALALA	GALSLSLAAG	AVAANKPASN	ATGVHKSAGH	SCGASKSAEG	SCGAAGSKAG
	10	20	30	40	50	60
	70	80	90	100		
a950.pep	EGKCGEGKCG	ATVKKTHKHT	KASKAKAKSA	EAGKC	EGKCG	GSKX
m950	EGKCGEGKCG	ATVKKTHKHT	KASKAKAKSA	EAGKC	EGKCG	GSK
	70	80	90	100		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2903>:
g951.seq

```

1 ATGATTATGT TACCCGCCCG TTTCACTATT TTATCTGTCC TCGCAGCAGC
51 CCTGCTTGCC GGACAGGGT ATGCTGCCGG CGCGCCGGAT GTGGAGCTGC
101 CGAAGGAAGT CGGAAGGTT TAAAGGAAAC ATCGCGTTA CAGCGAGGAA
151 GAAATCAAAA ACGAACCGC ACGGCTTGCG GCAGTGGCG AACGGGTCAA
201 CAGGGTGTTC ACGCTGTGG CGGGTGAACG GGCTTGCAG AAAGGGCAGG
251 CGGGAACGCC TCTGGCAACC TATATGCTGA TGTGGAAACG CACAAAATCC
301 CCCGAAGTCG CGAACGCCG CTTGGAAATG GCCGTGTCGC TGAACCGTT
351 TGAACAGGCC GAAATGATT ATCAGAAATG CGGGCAGATC GAGCCTATAC
401 CGGGTGGAGG GCAAAACGG CGGGGGTGGC TGCGGAACGT ATTGAGGGAA
451 GGGGGAAATC AGCATCTGGA CGGGTTGGAA GAGGTGCTGG CGCAATCGGA
501 CGATGTGCAA AACACGAGGA TATTTTGCT GCTGGTGCAA GCCGCCGTGC
551 AGCAGGGTGG GGTGGCTAA AAAGCATCGA AACCGGTTCG CCTGGCCGG
601 TTGAAGTATG AACATCTGCC CGAACGGCG GTTGCATG CGGTGTTCGG
651 CGTACAGGGG CGCAGAAAGG AAAAGGCAAT CGAACGTTTG CAGCGTTTG
701 CGAAGCTCGA TACGGAAATA TTGCCCCCCA CTTTAATGAC TTGCGTCTG
751 ACTGCACGCA AATATCCCAG AATACTCGAC GGCTTTTCG AGCAGACAGA
801 CACCCAAAAC CTTTCGGCG TCTGGAGGA AATGGAAATT ATGAATCTGG
851 TTTCCTGCG TAAGCCGGAT GATGCCATG CGCGTTGAA CGTGTGTTG
901 GAACACAACCG CGAATCCTAA CCTGTATATT CAGGCGGCGA TATTGGCGGC
951 AAACCGAAAAA GAAAGTGCCT CGGTATCGA CGCTACGCC GAAAAGGCAT
1001 ACGGCAGGGGG GACGGGGGA CAGCGGGCGA GGGCGGCAAT GACGGCGGGC
1051 ATGATATATG CCGACCGCAG GGATTACGCC AAAGTCAGGC AGTGGTTGAA
1101 AAAAGTGTCC GCGCCGGAAAT ACCTGTGCGA CAAAGGCCG CTGGCGGCTG
1151 CGGCCTGCG CGAAATTGGAC GGAGGCCGG CGGCTTGC CGAGATCGGC
1201 AGGGTGCAGGA AACTTCCCGA ACAGCAGGGG CGGTATTTTA CGGCAGACAA
1251 TTGTCCTAAA ATACAGATGC TCGCCCTGTC GAAGCTGCC GACAAACGGG
1301 AAGCCCTGAT CGGGCTGAAC AACATCATCG CCAAACCTTC GCGGGCGGG
1351 AGCACGGAAC CTTTGGCGGA AGCATTGGCA CAGCGTTCCA TTATTTACGA
1401 ACAGTTGCGG AAACGGGGAA AAATGATTGC CGACCTGAA ACCCGCGCTCA
1451 AACCTACGCC CGATAATGCA CAAATTATGA ATAATCTGGG CTACAGCCTG
1501 CTTTCGATT CCAAACGTTT GGACGAGGGT TTCCGCTGTC TTCAGACGCC
1551 ATACCAAATC AACCCGGACG ATACCGCCGT TAACGACAGC ATAGGCTGGG
1601 CGTATTACCT GAAAGGGGAC GCGGAAAGCG CGCTCCGTA TCTGCGGTAT
1651 TCGTTTGAAA ACGACCCCGA GCGCGAAGTT GCGCCCGATT TGGGCGAAGT
1701 GTGTTGGGCA TTGGGCGAAC GCGATCAGGC GTTGAACGTA TGGACGCGAG
1751 CGGCACACCT TAGGGGAGAC AAGAAAATAT GCGGGGAGAC GCTCAAACGC
1801 TACGGAATCG CCTTGCCCCGA GCCTTCCCGA AAACCCCGGA AATAA

```

This corresponds to the amino acid sequence <SEQ ID 2904; ORF 951.ng>:
g951.pep

```

1 MIMLPARFTI LSVLAAALLA QOAYAAGAAC VELPKEVGKV LRKHRRYSEE

```

51 EIKNERARLA AVGERVNRFV TLLGGETALQ KGQAGTALAT YMMLMLERTKS
 101 PEVAERALEM AVSLNAFEQA EMIYQKWRQI EPIPGEAQKR AGWLRNVLRE
 151 GGNQHLDGLE EVLAQSDDVQ KRRIFLLVQ AAVQQGGVVAQ KASKAVRRAA
 201 LKYEHLPEAA VADAVFGVQG REKEKAIEAL QRLAKLDTEI LPPTLMLTRL
 251 TARKYPEIIL GFFEQTDTQN LSAWQEMEI MNLVSLRKPD DAYARLNVLL
 301 EHNPANLYI QAAILAANRK EGASVIDGYA EKAYGRGTGE ORGRAAMTAA
 351 MIYADRRDYA KVRQWLKVKVS APEYLFDKGV LAAAAAAELED GGRAALRQIG
 401 RVRKLPEQQY RFYFTADNL SKIQLALSKLP DKREALIGLN NIIAKLSAAG
 451 STEPLAEALA QRSIYYEQFG KRGKMIADLE TALKLTPDNA QIMNNLGYSL
 501 LSDSKRLDEG FALLOTAYQI NPDDTAVNDs IGWAYYLKGD AESALPYLRY
 551 SFENDPEPEV AAHLGEVLWA LGERDQAVDV WTQAAHLRGD KKIWRETLKR
 601 YGIALPEPSR KPRK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2905>:

m951.seq

1 ATGATTATGT TACCTAACCG TTTCAAAATG TTAACCTGTG TGACGGCAAC
 51 CTTGATTGCC GGACAGGTAT CTGCCGCCGG AGGCAGGTGCG GGGGATATGA
 101 AACAGCCGA GGAAGCTCGA AAGCTTTCA GAAAGCAGCA GCGTTACAGC
 151 GAGGAAGAAA TCAAAACGA ACGCCACCGG CTTCGGCGAG TGGCGAGCG
 201 GGTAAATCAG ATATTCACGT TGCTGGAGG GGAACACCGCC TTGCAAAAGG
 251 GGCAGGCCGG AACGGCTCTG GCAACCTATA TGCTGATGTT GGAACGACA
 301 AAATCCCCCG AAGTCGCCGA ACGCCCTTG GAAATGGCCG TGTCGCTGAA
 351 CGCGTTTGA CAGGCAGGAA TGATTATCA GAAATGGCGG CAGATTGAGC
 401 CTATACCGGG TAAGGCAGCA AACCGGGCGG GTGGGCTGCC GAACGTGCTG
 451 AGGGAAAGAG GAAATCAGCA TCTGGACCGGA CTGGAAGAAG TGCTGGCTCA
 501 GGCAGCACAA GGACAGAACCG CAAGGGTGTG TTATTGTTG GCACAAGCCG
 551 CCGTGCAACA GGACGGGTTG GCGCAAAAG CATCGAAAGC GGTTCGCCG
 601 GCGGCCTTGA AATATGAACA TCTGCCGAA GCGGCCTTGC CCGATGTGGT
 651 GTTCAGCGT CAGGGCAGCG AAAAGGAAAA GCGAATCGGA GCTTTCAGC
 701 TTTTGGCGAA GCTCGATACG GAAATATTGC CCCCCACTTT AATGACGTTG
 751 CGTCTGACTG CACGCAAATA TCCCGAAATA CTCGACGGCT TTTTCGAGCA
 801 GACAGACACC CAAAACCTT CGGCCGCTCTG GCAGGAAATG GAAATTATGA
 851 ATCTGGTTTC CCTGCACAGG CTGGATGATG CCTATGCGCG TTTGAACGTG
 901 CTGTTGGAAAC GCAATCCGAA TCGCACCTG TATATTCAAGG CAGCAGTATT
 951 GGGGGCAAC CGAAAAGAAG GTGCTCCGT TATCGACGGC TACGCCGA
 1001 AGGCATACGG CAGGGGGACG GAGGAACAGC GGAGCAGGGC GGCCTAACG
 1051 GCGGCATGTA TGTATGCCG CCGCAGGGAT TAGCCTAACAG TCAGGCAGTG
 1101 GCTAAAAAA GTATCCGCGC CGGAATACCT GTTCGACAAA GGTGTGCTGG
 1151 CGGCTGCGGC GGCTGTCGAG TTGGACGGCG GCAGGGCGGC TTTGCAGC
 1201 ATCGGCAGGG TCGGAAACT TCCCGAACAG CAGGGGCCGT ATTTCAGGC
 1251 AGACAATTG TCCAAAATAC AGATGCTCGC CCTGTCGAAG CTGCCGATA
 1301 AACGGGAGGC TTGAGGGGG TTGGACAAAGA TTATCGAAAA ACCGCCTGCC
 1351 GGCAGTATAA CAGAGTTACA GGCAGAGGCA TTGGTACAGC GGTCACTTG
 1401 TTACGATCGG CTTGGCAAGC GGAAAAAAAT GATTCAGAT CTTGAAAGGG
 1451 CGTTCAAGCT TGCACCCGAT AACGCTCAGA TTATGAATAA TCTGGCTAC
 1501 AGCCTGCTGA CCGATTCCA ACGTTGGAC GAAGGTTTCG CCCTGCTTCA
 1551 GACGGCATAC CAAATCAACC CGGACGATAC CGCTGTCAC GACAGCATAG
 1601 GCTGGGCGTA TTACCTGAAA GGCAGCGCG AAAGCGCGCT GCCGTATCTG
 1651 CGGTATTCTG TTGAAAACGA CCCCAGGCCA GAAGTGGCCG CCCATTGGG
 1701 CGAAGTGTG TGGGCATTGG GCGAACCGCA TCAGGCGTT GACGTATGGA
 1751 CGCAGGGCGGC ACACCTAACG GGAGACAAGA AAATATGGCG GGAAACGCTC
 1801 AAACGTCACG GCATCGCATT GCCCCAACCT TCCCGAAAAC CTCGGAAATA
 1851 A

This corresponds to the amino acid sequence <SEQ ID 2906; ORF 791>:

m951.pep

1 MIMLPNRFKM LTVLTATTLLIA GQVSAAGGGA GDMKQPKEVG KVFRKQQRYS
 51 EEEIKNERAR LAAVGERVNQ IFTLLGGETA LQKGQAGTAL ATYMLMLERT
 101 KSPEVAERAL EMAVSLNAFE QAEIMYQKWR QIEPIPGKAQ KRAGWLRNVL
 151 RERGNQHLDG LEEVLAQADE QONRRVFLLL AOAAVQQDGL AQKASKAVRR
 201 AALKYEHLPE AAVADVVFVSV QGREKEKAIG ALQRLAKLDT EILPPTLML
 251 RLTARKYPEI LDGFFEQTDT QNLSAVWQEM EIMNLVSLHR LDDAYARINV
 301 LLERNPNADL YIQAAILAAAN RKEGASVIDG YAEKAYGRGT EEQRSRAALT
 351 AAMMYADRRD YAKVRQWLKK VSAPELYFDK GVIAAAAAME LDGGRAALRQ
 401 IGRVRLPEQ OGRYFTADNL SKIQLALSKLP DKPKREALRG LDKIIEKPPA
 451 GSNTTELQAEA LVQRSVVYDR LGKRKKMISD LERAFLRAPD NAQIMNNLGY
 501 SLLTDSKRLD EGFALLQTAQ QINPDDTAVN DSIGWAYYLK GDAESALPYL
 551 RYSFENDPEP EVA AHLGEVL WALGERDQAV DVWTQAAHLT GDKKIWRETL
 601 KRHGIALPOF SRKPRK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 951 shows 88.6% identity over a 616 aa overlap with a predicted ORF (ORF 951) from *N. gonorrhoeae*

m951/g951 88.6% identity in 616 aa overlap

m951.pep	10	20	30	40	50	60
	MIMLPNRFKMLTVLTLATLIAGQVSAAGGGAGDMKQPKEVGKVFRKQQRYSSEEIKNERAR	: : : : : : : : : : : : : : : : : : : :				
g951	10	20	30	40	50	
	MIMLPARFTILSVLAALLAGQAYAA--GAADVELPKEVGKVLRKHRRYSEEIKNERAR	: :				
m951.pep	70	80	90	100	110	120
	LAAVGERVNQIFTLLGGETALQKGQAGTALATYMLMLERTKSPEVAERALEMAVSlnafe	: : : : : : : : : :				
g951	60	70	80	90	100	110
	LAAVGERVNVRVFTLLGGETALQKGQAGTALATYMLMLERTKSPEVAERALEMAVSlnafe	: : : : : : : : : :				
m951.pep	130	140	150	160	170	180
	QAEMIYQKWRQIEPIPGKAQKRAGWLRLNRVLREGNQHLDGLEEVLAQADEGQNRRVFLLL	: : : : : : : : : :				
g951	120	130	140	150	160	170
	QAEMIYQKWRQIEPIPGEAQKRAGWLRLNRVREGGNQHLDGLEEVLAQSDDVQKRRIFLLL	: : : : : : : : : :				
m951.pep	190	200	210	220	230	240
	AQAAVQQDGLAQKASKAVRRAALKYEHLPAAVADVVFSVQGREKEKAIGALQRLAKLDT	: : : : : : : : : : :				
g951	180	190	200	210	220	230
	VQAAVQQGGVAQKASKAVRRAALKYEHLPAAVADAVFGVQGREKEKAIEALQRLAKLDT	: : : : : : : : : : :				
m951.pep	250	260	270	280	290	300
	EILPPPTLMTRLTARKYPEILDGFFEQTDTQNLSAVWQEMEIMNLVSLHRLDDAYARLN	: : : : : : : : : : :				
g951	240	250	260	270	280	290
	EILPPPTLMTRLTARKYPEILDGFFEQTDTQNLSAVWQEMEIMNLVSLRKPDAYARLN	: : : : : : : : : : :				
m951.pep	310	320	330	340	350	360
	LLERNPNADLYIQAAILAAANRKEGASVIDGYAEKAYGRGTEEQRSRAALTAAMMYADRRD	: : : : : : : : : : :				
g951	300	310	320	330	340	350
	LLEHNPNANLYIQAAILAAANRKEGASVIDGYAEKAYGRGTEQRGRAAMTAAMIYADRRD	: : : : : : : : : : :				
m951.pep	370	380	390	400	410	420
	YAKVRQLKKVSAPEYLFDKGVLAAAALVEDGGRAALRQIGRVRKLPEQQGRYFTADNL	: : : : : : : : : : :				
g951	360	370	380	390	400	410
	YAKVRQLKKVSAPEYLFDKGVLAAAALVEDGGRAALRQIGRVRKLPEQQGRYFTADNL	: : : : : : : : : : :				
m951.pep	430	440	450	460	470	480
	SKIQMLALSKLPDKREALRGLDKIIEKPPAGSNTELQAEALVQRSVVDRLGKRKKMISD	: : : : : : : : : : :				
g951	420	430	440	450	460	470
	SKIQMLALSKLPDKREALIGLNNIIAKLSAAGSTEPLAALAQRSIIYEQFGKRGKMIAD	: : : : : : : : : : :				
m951.pep	490	500	510	520	530	540
	LERAFLRAPDNAQIMNNNLGYSLLTDSKRLDEGFALLQTAYQINPDDTAVNDSIGWAYYLK	: : : : : : : : : : :				
g951	480	490	500	510	520	530
	LETALKLTPDNAQIMNNNLGYSLSDSKRLDEGFALLQTAYQINPDDTAVNDSIGWAYYLK	: : : : : : : : : : :				
m951.pep	550	560	570	580	590	600
	GDAESALPYLRYSFENDPEPEVA AHLGEVLWALGERDQAVDVWTQAAH LTGDKKIWR	: : : : : : : : : : :				
g951	540	550	560	570	580	590
	GDAESALPYLRYSFENDPEPEVA AHLGEVLWALGERDQAVDVWTQAAH LRGDKKIWR	: : : : : : : : : : :				
m951.pep	610					
	KRHGIALPOPSRKPRK	: : : : : : : : : : : : : : :				
g951	600	610				
	KRYGIALPEPSRKPRK	: : : : : : : : : : :				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2907>:
a951.seq

1	ATGTTACCCG	CCCGTTTCAc	CATTTTATCT	GTGCTCGGG	CAGCCCTGCT
51	TGCCGGGCAG	GCGTATGCG	CCGGCGCGC	GGATGCGAA	CCGCCGAAGG
101	AAGTCGGAAA	GGTTTTCAGA	AAGCAGCAGC	GTTACAGCGA	GGAAGAAATC
151	AAAAAACGAAc	GGCGCACGGT	TGGCGACTGG	GGCGAGCGGG	TTAATCAGAT
201	ATTACGTTG	CTGGGAGGGG	AAACCGCCCT	GCAAAAGGGG	CAGGCGGGAA
251	CGGCTCTGGC	AACCTATATG	CTGATGTTGG	AACGCAACAA	ATCCCCCGAA
301	GTCGCCGAAC	GCGCCTTGG	AATGGCGGTG	TCGCTGAACCG	CGTTGAAACA
351	GGCGGAAATG	ATTATCAGA	AATGGCGGCA	GATTGAGCC	ATACC GG GT A
401	AGGGCGAAAA	ACGGGGGGGG	TGGCTGCGGA	ACGTGCTGAG	GGAAAGAGGA
451	AATCAGCATC	TAGACGGACT	GGAGAGAAGTG	CTGGCTCAGG	CGGACGAAGG
501	ACAGAACCGC	ACGGGTGTTT	TATTGTTGGC	ACAAGCGGCC	GTGCAACAGG
551	ACGGGTTGGC	GCAAAAAGCA	TCGAAAGCGG	TCGCGCCGCG	GGCGTTGAGA
601	TATGACATC	TGCCCAGAAC	GGCGGTTGCG	GATGTTGGTGT	TCAGCGTACA
651	GGGACCGGAA	AAGGAAAGG	CAATCGGAGC	TTTGCAGCGT	TTGGCGAAGC
701	TCGATACGG	AATATTGCC	CCCAACTTAA	TGACGTTGCG	TCTGACTGCA
751	CGCAAATATC	CCGAAATACT	CGACGGCTTT	TTCGAGCAGA	CAGACACCCA
801	AAACCTTTG	GCCGTCGCG	AGGAATGG	AATTATGAAT	CTGGTTTCCC
851	TGACACAGGCT	GGATGATGCC	TATGCGCGTT	TGAACGTGCT	GTGGAACCG
901	AATCCGAATG	CGACAGCTGA	TATTCAAGCA	GGGATATTGG	CGGCAAACCG
951	AAAAAGAGGT	GCTTCCGTTA	TCGACGGCTA	CGCCGAAAAG	GCATACGGCA
1001	CGGGGGACGGG	GGAACAGCGG	GGCAGGGCGG	CAATGACGCC	GGCGATGATA
1051	TATGCCGACC	GAAGGGATT	CACCAAAGTC	AGGCAGTGGT	TGAAAAAAAGT
1101	GTCCCGCGCC	GAATACCTGT	TCGACAAAGG	TGTGCTGGCG	GCTCCGGCGG
1151	CTGTCGAGT	GGACGGCGGG	AGGGCGGCTT	TGGCGCAGAT	CGGCAGGGTG
1201	CGGAAACTTC	CCGAAACAGCA	GGGGCGGTAT	TTTACGGCAG	ACAATTGTC
1251	CAAATAACAG	ATGTCGCCCC	TGTCGAAGCT	GGCCGCACAAA	CGGGAGGCTT
1301	TGAGGGGGTT	GGACAAGATT	ATCGAAAAAAC	CGCGCTCGCG	CAGTAATACA
1351	GAGTTACAGG	CAGAGGCATT	GGTACAGCGG	TCAGTTGTTT	ACGATCGGCT
1401	TGGCAACGG	AAAAAAATGA	TTTCAGATCT	TGAAAGGGCG	TTCAGGCTTG
1451	CACCCGATAA	CGCTCAGATT	ATGAAATACT	TTGGGCTACAG	CCTGCTTCC
1501	GATTCCAAAAC	GTTTGGACGA	AGGCTTCGCC	CTGCTTCAGA	CGGCATACCA
1551	ATATCAACCG	GACGATAACCG	CTGTCACAGA	CAGCATAGGC	TGGGCGTATT
1601	ACCTGAAAGG	CGACGGGGAA	AGCGCGCTGC	CGTATCTGCC	GTATTCTGTT
1651	AAAAAACGAC	CCGAGCCCCG	AGTTGCCGCC	CATTGGGCG	AAGTGTGTTG
1701	GGCATGGGC	GAACGCCATC	AGGGCGGTGA	CGTATGGACG	CAGGCAGGAC
1751	ACCTTACGGG	AGACAAGAAA	ATATGGCGGG	AAACGCTCAA	ACGTCAACGGC
1801	ATCGCATTGC	CCCCAACCTTC	CGGAAAACCT	CGGAAAATAA	

This corresponds to the amino acid sequence <SEO ID 2908: ORF 951_a>.

a951.pep

```

1 MLLPARFTILS VLAAGALLAGQ AYAAGAAADAK PPKEVGKVFR KQQRYSSEEEI
51 KNERARLAAV GERVNQIFTL LGGETALQKG QAGTALATYM LMLERTKSP
101 VAERALEMAV SLNAFEQAEM IYQKWRQIEP IPGKAQKRAG WLRLNVLRERG
151 NOHLDGLEEV LAQADEGQNRR RVFLLLAQAA VQQDGLAQKA SKAVRRAALR
201 YEHLPEAAVA DVVFSVQGRE KEKAIGALQR LAKLDTEILP PTLMTLRLTA
251 RKYPEILDFF FEQTDTQNLSS AVWQEMEIMN LVSLHRLDDA YARLNVLLER
301 NPNAIDLVIQA AILAANRKEG ASVIDGYAEK AYGRGTGEQR GRAAMTAAMI
351 YADRRTDYTKV RQWLKKVKSAP EYLFDKGVLAA AAAVELDDG RAALRQIGRV
401 RKLPEQQGRY FTADNLSKIQ MFALSKLPDK REALRGLDKI IEKPPAGSNT
451 ELQAEALVQR SVVYDRRLGKRR KKMISDLERA FRLAPDNAQI MNNLGYSSL
501 DSKRRLDEGFA LLQOTAYQINP DDTAVNDSIG WAYYLKGDAE SALPYLRYSF
551 ENDPPEVAAA HLGEVWLWALG ERDQAVDVWT QAAHLTGDKK IWRETLKRGH
600 IALPOPSRKK BK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 951 shows 96.4% identity over a 614 aa overlap with a predicted ORF (ORF 951) from *N. meningitidis*.

a951/m951 96.4% identity in 614 aa sequence

	10	20	30	40	50
a951.pep	MLPAREFTILSVLAAALLLAGQAYAAG--AADAKPPKEVGKVFRKQQRYSEEEEIKNERAR	: : : : :			
m951	MIMLPNRFKMLTVLTATLIAGQVSAAGGGAGDMKQPKEVGKVERKOORYSEEEIKNERAP	: : : : :			

a951.pep 60 LAAVGERVNOIFTLLGGETALOKGOAGTALATYMI MLFPTKSGPENIPLR 110

m951	LAAVGERVNQIFTLLGGETALQKGQAGTALATYMLMLERTKSPEVAERALEMVASLNafe 70 80 90 100 110 120									
a951.pep	120	130	140	150	160	170	QAEMIYQKWRQIEPIPGKAQKRAGWLRNVLRERGNQHLDGLEEVLAQADEGQNRRVFLLL			
m951	QAEMIYQKWRQIEPIPGKAQKRAGWLRNVLRERGNQHLDGLEEVLAQADEGQNRRVFLLL 130 140 150 160 170 180									
a951.pep	180	190	200	210	220	230	AQAAVQQDGLAQMKAASKAVRRAALRYEHLPEAAVADVVFSVQGREKEKAIGALQRLAKLDT			
m951	AQAAVQQDGLAQMKAASKAVRRAALKYEHLPEAAVADVVFSVQGREKEKAIGALQRLAKLDT 190 200 210 220 230 240									
a951.pep	240	250	260	270	280	290	EILPPTLMTLRLTARKYPEILDGFFEQTDTQNLSAVWQEMEIMNLVSLHRLDDAYARLNV			
m951	EILPPTLMTLRLTARKYPEILDGFFEQTDTQNLSAVWQEMEIMNLVSLHRLDDAYARLNV 250 260 270 280 290 300									
a951.pep	300	310	320	330	340	350	LLERNPNADLYIQAAAILAANRKEGASVIDGYAEKAYGRGTGEQRGRAAMTAAMMYADRRD			
m951	LLERNPNADLYIQAAAILAANRKEGASVIDGYAEKAYGRGTTEEQRSSRAALTAAAMMYADRRD 310 320 330 340 350 360									
a951.pep	360	370	380	390	400	410	YTKVRQWLKKVSAPEYLFDKGVLAAAAAVELDGGRAALRQIGRVRKLPEQQGRYFTADNL			
m951	YAKVRQWLKKVSAPEYLFDKGVLAAAAAVELDGGRAALRQIGRVRKLPEQQGRYFTADNL 370 380 390 400 410 420									
a951.pep	420	430	440	450	460	470	SKIQMFAKSLPKDKREALRGLDKIIIEKPPAGSNTTELQAEALVQRSVVDRLGKRKKMISD			
m951	SKIQMFLAKSLPKDKREALRGLDKIIIEKPPAGSNTTELQAEALVQRSVVDRLGKRKKMISD 430 440 450 460 470 480									
a951.pep	480	490	500	510	520	530	LERAFLRAPDNAQIMNNLGYSLLSDSKRLDEGFALLQTAYQINPDDTAVNDSIGWAYYLK			
m951	LERAFLRAPDNAQIMNNLGYSLLSDSKRLDEGFALLQTAYQINPDDTAVNDSIGWAYYLK 490 500 510 520 530 540									
a951.pep	540	550	560	570	580	590	GDAESALPYLRYSFENDPEPEVA AHLGEVLW ALGERD QAVDVWTQAAH LTGD KKI WRE TL			
m951	GDAESALPYLRYSFENDPEPEVA AHLGEVLW ALGERD QAVDVWTQAAH LTGD KKI WRE TL 550 560 570 580 590 600									
a951.pep	600	610	KRHGIALPQPSRKPRK							
m951	KRHGIALPQPSRKPRK 610									

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2909>:
 g952.seq (partial)

```

1 ..TTGTCTTATC GTTTGAATGC TGCACCGATG TTTAACGATA ATCCCTGTTG
51 TTACGGAAA ATCAAATTGC AGAGTTGGAA AGCGCGGCCG GATTTCAATA
101 TTGTAAAGCA GGATTTCGAT TTTCTCTGCG GGGCGGCCCTC GGTGGCGACG
151 CTTTTGAACA ATTTTACGG GCAGAAAGCTG ACGGAAGAAG AAGTGTGGA
201 AAAACTGGGT AAGGAACAGA TGCGCGCGTC GTTGAGGAT ATGCGGCAGCA
251 TTATGCCCGA TTGGGTTTT GAGGCAGAAAG CCTATGCCCT GTCTTTCGAA
301 CAGCTCGCGC AGTTGAAAAT CCCCGTCATC GTGTATCTGA AATACCGCAA
351 AGACGACCAT TTTTCCGTAT TGCGCGGAGT GGATGGCAAT ACGGTTTTGC
401 TTGCGCACCC GTGCCGGGGT CATGTTTCGA TGAGCAGGGC GCAGTTTTG
451 GAGGCTTGGC AAACCCGCTGA GGGAAATTTC GCAGGGCAAAA TTTTGGCGGT
501 CGTGCGGAAA AAACCGGGAGG CGATTTCAAA TAAATTGTTT TTCACACATC
551 ATCCCAAGCG GCAGACGGAG TTTGCGACTCG GACAGGTAAA ATGGTGGCGT

```

601 GCTTATTGA

This corresponds to the amino acid sequence <SEQ ID 2910; ORF 952.ng>:

g952.pep (partial)

```

1 ..LSYRLNAAPM FNDNPVYVGK IKLQSWKARR DFNIVKQDLD FSCGAASVAT
51 LLNNFYGQKL TEEEVLEKLG KEQMRAFSFED MRRIMPDLGF EAKGYALSFE
101 QLAQLKIPVI VYLYRKDDH FSVLRGVDG D TVLLADPSPG HVSMSRAQFL
151 EAWQTREGNL AGKILAVVPK KAEAISNKLF FTHHPKRQTE FAVGQVKWWWR
201 AY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2911>:

m952.seq

```

1 ATGATGAAGT TCAAATATGT TTTCTGTTG GCGTGTGTTG TCGTTCTTT
51 ATCTTATCGT TTGAATGCTG CACCGATGTT TAACGATAAT CCTGTTGTTT
101 ACGGAAAAT CAAAGTCGAG AGTTGAAAG CGCGCCGGGA TTCAATATT
151 GTAAAGCAGG ATTGGGATT TTCTCTGGG CGCGCTTCGG TGCGCACGCT
201 TTTGAACAAT TTTTACGGGC AAACGCTGAC GGAAGAAGAA GTGTTGAAAA
251 AGCTGGATAA GGAGCAGATG CGCGCGTCGT TTGAGGATAT GCGGCGCATT
301 ATGCTCTGATT TGGGTTTGA GGCAGAAGGGC TATGCCCTGT CTTTCGAGCA
351 GCTCGCCGAG TTGAAATACCC CGCTCATCGT GTATCTGAAA TACCGCAAAG
401 ACGACCAATT TTCGGTATTG CGCGGTATAG ACGGCAATAC GGTTTTGCTT
451 GCCGACCCGT CGCTGGGCA TGTTCAATG AGCAAGGGCG AGTTTTTGGA
501 TGCTTGGCAA ACCCGTGAAGG GAAATTTGGC AGGTAAAGATT TTGGCTGTCA
551 TACCGAAAAA AGCCGAGACA ATTTCAAATA AATTGTTTTT CACACAAACAC
601 CCAAAACGGC AGACGGAGTT TACAGTCGGA CAAATCAGGC AAGCACGTGC
651 AGAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2912; ORF 952>:

m952.pep

```

1 MMKFKYVFL ACVVVSLSYR LNAAPMFNDN P VVYKGKIKVQ SWKARRDFNI
51 VKQDLDLDFSCG AASVATLLNN FYQQLTEEE VLKKLDKEQM RASFEDMRRI
101 MPDLGFEAKG YALSFQLAQ LKIPVIVYLK YRKDDHFSVL RGIDGNTVLL
151 ADPSLGHVSM SRAQFLDAWQ TREGNLAGKI LAVIPKKAET ISNKLFFTQH
201 FKQTEFTVQ QIRQARAE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 952 shows 92.5% identity over a 201 aa overlap with a predicted ORF (ORF 952) from *N. gonorrhoeae*

g952/m952; 92.5% identity in 201 aa overlap

g952.pep m952	10 20 30 40 LSYRLNAAPMFNDNPVYVGKIKLQSWKARRDFNIVKQDLDLDFSCG : : : : : : : MMKFKYVFLACVVVSLSYRLNAAPMFNDNPVYVGKIKVQSWKARRDFNIVKQDLDLDFSCG 10 20 30 40 50 60
g952.pep m952	50 60 70 80 90 100 AASVATLLNNFYGQKLTEEEVLEKLGKEQMRAFSFEDMRRIMPDLGFEAKGYALSFEQLAQ : : : : : : AASVATLLNNFYGQKLTEEEVLEKLGKEQMRAFSFEDMRRIMPDLGFEAKGYALSFEQLAQ 70 80 90 100 110 120
g952.pep m952	110 120 130 140 150 160 LKIPVIVYLYRKDDHFSVLRGVDGNTVLLADPSPGHVMSRAQFLEAWQTREGNLAGKI : : : : : : LKIPVIVYLYRKDDHFSVLRGVIDGNTVLLADPSLGHVMSRAQFLDAWQTREGNLAGKI 130 140 150 160 170 180
g952.pep m952	170 180 190 200 LAVVPKKAEAIISNKLFFTHHPKRQTEFAVGQVKWWRAYX : : : : : : LAVIPKKAETISNKLFFTHHPKRQTEFTVGQIRQARAE 190 200 210

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2913>:

a952.seq

```

1 ATGATGAAGT TCAAATATGT TTTCTGTTG GCGTGTGTTG TCGTTCTTT

```

```

51 ATCTTATCGT TTGAATGCTG CACCGATGTT TAACGATAAT CCTGTTGTTT
101 ACGGAAAAAT CAAAGTGCAG AGTTGAAAG AAAGGCGGGA TTTCAATATT
151 GTAAAGCAGG ATTTGGATTTCCTCGGG GCGGCTTCGG TGGCGACGCT
201 TTGAAACAAT TTTTACGGGC AACACGTGAC GGAAGAAGAA GTGTTGAAA
251 AGCTGGATAA GGAGCAGATG CGCCCGTCGT TTGAGGATAT CGGGCGCATT
301 ATGCCAGATT TGGGTTTGAGCAGAAAGGC TATGCCCTGT CTTTCGAGCA
351 GCTCGCACAG TTGAAAATCC CCGTCATCGT GTATCTGAAA TACCGCAAGG
401 ATGATCATTT CTGCGTATTG CGCGGGATAG ACGGCAATAC GGTTTTGCTT
451 GCCGACCCGT CGCTGGGTCA TGTTCAATG AGCAGGGCGC AGTTTTNGGA
501 TGCTTGGCAA ACCCGTGAGG GAAATTGAGC AGGTAAGATT TTGGCGGTG
551 TGCCGAAAAA AGCCGAGACA ATTICAAATA ATTTGTTT CACACATCAT
601 CCCAACGGGC AGACGGAGTT TGCACTCGGA CAAATCAGGC AAGCACGTGC
651 AGAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2914; ORF 952.a>:

a952.pep

```

1 MMKFKYVFL ACVVVSLSYR LNAAPMFNDN PVVYGKIKVQ SWKERRDFNI
51 VKQDLDLDFSCG AASVATLNN FYGQTLTEEE VLKKLDKEQM RASFEDMRRI
101 MPDLGFEAKG YALSFEQLAQ LKIPVIVYLN YRKDDHFSVL RGIDGNTVLL
151 ADPSLGHVSM SRAQFXDAWQ TREGNLAGKI LAVVPKKAET ISNKLFPTHH
201 PKRQTEFAVG QIRQARAE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 952 shows 97.7% identity over a 218 aa overlap with a predicted ORF (ORF 952) from *N. meningitidis*

a952/m952 97.7% identity in 218 aa overlap

a952.pep	10	20	30	40	50	60
	MMKFKYVFL ACVVVSLSYR LNAAPMFNDN PVVYGKIKVQ SWKERRDFNI	VKQDLDLDFSCG				
m952	10	20	30	40	50	60
	MMKFKYVFL ACVVVSLSYR LNAAPMFNDN PVVYGKIKVQ SWKERRDFNI	VKQDLDLDFSCG				
a952.pep	70	80	90	100	110	120
	AASVATLNNFYGQTLTEEEVLKKLDKEQM RASFEDMRIMPDLGFEAKGYALSFEQLAQ					
m952	70	80	90	100	110	120
	AASVATLNNFYGQTLTEEEVLKKLDKEQM RASFEDMRIMPDLGFEAKGYALSFEQLAQ					
a952.pep	130	140	150	160	170	180
	LKIPVIVYLKYRKDDHFSVLRGIDGNTVLLADPSLGHVSMMSRAQFXDAWQTREGNLAGKI					
m952	130	140	150	160	170	180
	LKIPVIVYLKYRKDDHFSVLRGIDGNTVLLADPSLGHVSMMSRAQFLDAWQTREGNLAGKI					
a952.pep	190	200	210	219		
	LAVVPKKAETISNKLFPTHHPKRQTEFAVGQIRQARAE					
m952	190	200	210			
	LAVIPKKAETISNKLFPTQHPKRQTEFTVGQIRQARAE					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2915>:
g953.seq

```

1 ATGAAAAAAA TCATCTTCGC CGCGCTCGCA GCAGCGCCG TCGGCACTGC
51 CTCGCCACC TACAAAGTGG ACCAATATCA CGCCAACGTC CGTTTCGCCA
101 TCGACCACTT CAACACCAGC ACCAACGTGCG GCGGTTTTA CGGTCTGACC
151 GTTCCCGTCG AGTCGATCA AGCAAAACGC GACGGCAAAA TCGACATCAC
201 CATTCCCGTC GCCAACCTGC AAAGCGGTTC GCAACCTTC ACCGGCCACC
251 TGAATCCGC CGACATCTTC GATGCCGCTC AATATCCGGA CATCCGCTTC
301 GTTCCACCA AATTCAACTT CAACGGCAA AAACTTGTGTTT CGGTTGACGG
351 CAACCTGACC ATGCGCGGCA AAACCGCCCC CGTCAAAACTC AAAGCCGAAA
401 AATTCAACTG CTACCAAAGC CCGATGGCGG AAACCGAAGT TTGGCGCGGC
451 GACTTCAGCA CCACCATCGA CCGCACCAA TGGGGCGTGG ACTACCTCGT
501 TAACGCCGGT ATGACCAAAA ACGTCCGCAT CGACATCCAA ATCGAAGCTG
551 CAAACAAATA A

```

This corresponds to the amino acid sequence <SEQ ID 2916; ORF 953.ng>:
g953.pep

```

1 MKKIIIFAAAL AAAVGTASAT YKVDEYHANV RFAIDHFNTS TNVGGFYGLT
51 GSVEFDOAKR DGKIDITIPV ANLQSGSQPF TGHLKSADIF DAAQYPDIRF
101 VSTKFNFGK LKLVSVDGNL MRGKTPAVKL KAEKFNCYQS PMAETEVCGG
151 DFSTTIDTRK WGVGDYLVNAG MTKNVRIDIO IEAAKO*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2917>:

m953.seq

```

1 ATGAAAAAAA TCATCTTCGC CGCACTCGCA GCGCCGCGCA TCAGTACTGCG
51 CTCCGCCGCC ACCTACAAAG TGGACGAATA TCACGCCAAC GCGCGTTTCG
101 CCATCGACCA TTTCAACACC AGCACCAACG TCGGGGTTT TTACGGTCTG
151 ACCGGTTCGG TCGAGTTCGA CCAAGCAAA CGCGACGGTA AAATCGACAT
201 CACCATCCCCC ATTGCGAACAC TCGAAAGCGG TTCCGAAACAC TTACCGGAC
251 ACCTGAAATC AGGCGCACATC TTTCGATTCGG CCCAATATCCG GGCACATCCG
301 TTTGTTTCCA CCAAATTCAA CTTCAACCGG AAAAAACTGG TTTCGGTTGA
351 CGGCAACCTG ACCATGCACG GCAAAACCGC CCCCCTCAA CTCAAAGCCG
401 AAAAAATTCAA CTGCTACCAA AGCCCCATGG AGAAAACCGA AGTTTGTGGC
451 GGGCACTCA GCACCCACCAT CGACCCGACCC AAATGGGGCA TGGAACACCT
501 CGTTAACCGT GGTATGACCA AAAGCGTCCG CATCGACATC CAAATCGAGG
551 CAGGGAAACA ATAAT

```

This corresponds to the amino acid sequence <SEO ID 2918: ORE 953>:

m953.pep

1 MKKIIIFAALA AAAISTASAA TYKVDEYHAN ARFAIDHFNT STNVGGFYGL
51 TGSVFEDQAK RDGKIDITIP IANLQSQSH FTDHLKSADI FDAAQYPDIR
101 FVSTKFNFRT KKLVSVDGNL TMHGKTAPOVK LKAEKFNCYQ SMEKTEVCG
151 GDSTTIDTR KWGMGYDLVNV GMTKSVRIDI OIKAOK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 953 shows 93.0% identity over a 187 aa overlap with a predicted ORF (ORF 953) from *N. gonorrhoeae*.

m953/g953 93.0% identity in 187 aa overlap

m953.pep	10	20	30	40	50	60		
	MKKIIFAA L AAAISTASAATYKVDEYHANARFAIDHFNTSTNVGGFYGLTGSVEFDQAK	: : : : : : : : : : :						
g953	MKKIIFAA L AAA V GTASA-TYKVDEYHANVRAIDHFNTSTNVGGFYGLTGSVEFDQAK	: : : : : : : : : : :	10	20	30	40	50	
m953.pep	70	80	90	100	110	120		
	RDGKIDITIPIANLQSGSQHFTDHLKSADIFDAAQYPDIRFVSTKFNFNGKKLVSDGNL	: : : : : : : : : : :						
g953	RDGKIDITIPVANLQSGSQPFTGHLKSADIFDAAQYPDIRFVSTKFNFNGKKLVSDGNL	: : : : : : : : : : :	60	70	80	90	100	110
m953.pep	130	140	150	160	170	180		
	TMHGKTAPVKLKA E KFNCYQSPMEKTEVC G DFSTTIDRTK W GMDYLVNVGMTKSVRIDI	: : : : : : : : : : :						
g953	TMRGKTAPVKLKA E KFNCYQSPMAETEVCG G DFSTTIDRTK W GV D YLVAGMTK N VRIDI	: : : : : : : : : : :	120	130	140	150	160	170
m953.pep	QIEAAKQX							
g953	QIEAAKQX							
	180							

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2919>:
a953.seq

1

1 ATGAAAAAAA TCATCATCGC CGCGCTCGCA GCAGCCGCCA TCGGCAC TGC
51 CTCCGCCGCC ACCTTACAAAG TGGACGAATA TCACGCCAAC GCCC GTT TCT
101 CTATCGACCA TTTCACCAACC AGCACCAACG TCGCGGT TTT TACCGTCTG
151 ACCGGTTCCG TTGAGTTCGA CCAAGCAAAA CGCGACGGTA AAATCGACAT
201 CACCATCCCC GTTGCCAAACC TGCAAAGCGG TTGCAACAC TTACCGACCC
251 ACCTGAAATC AGCCGACATC TTGATGCCG CCCAATATCC GGACATCGC
301 TTTGTTTCCA CCAAATTCA CTTCAACGGC AAAAAACTGG TTCCGGTTGA

```

351 CGGCAACCTG ACCATGCACG GCAAAACCGC CCCCCGTCAA  CTCAAAGCCG
401 AAAAATTCAA CTGCTACCAA AGCCCCATGT TGAAAACCAGA AGTTTGCGGC
451 GGGCACTTCG ACACCCACCAT CGACCCGACCC AAATGGGGCA TGGACTACCT
501 CGTTAACCGT GGTATGACCA AAAGCGTCCG CATCGACATC CAAATCGAGG
551 CAGCCAAACA ATAA

```

This corresponds to the amino acid sequence <SEO ID 2920: QRE 953 a>.

a953.pep

1 MKKIIIAALA AAAIGTASAA TYKVDEYHAN ARFSIDHFNT STNVGGFYGL
51 TGSVEFDQAK RDGKIDITIP VANLQSQSQH FTDHLKSADI FDAAQYPDIR
101 FVSTKFNFNG KKLVSVDGNL TMHGKTAPVK LKAEKFNCYQ SPMLKTEVCG
151 GDFSTTIDRT KWGMMDLVNV GMTKSVRIDI QIEAAKO*

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. meningitidis*.

ORF 953 shows 97.3% identity over a 187 aa overlap with a predicted ORF (ORF 953) from *N. meningitidis*.

a953/m953 97.3% identity in 187 aa overlap

a953.pep	10	20	30	40	50	60		
	MKKIIIAAALAAAAIGTASAATYKVDEYHANARFSIDHFNTSTNVGGFYGLTGSVEFDQAK	: : : : : : : : : : :						
m953	MKKIIFAAALAAAAISTASAATYKVDEYHANARFAIDHFNTSTNVGGFYGLTGSVEFDQAK	: : : : : : : : : : :	10	20	30	40	50	60
a953.pep	70	80	90	100	110	120		
	RDGKIDITIPVANLQSGSQHFTDHLKSADIFDAAQYPDIRFVSTKFNFNGKKLVSVDGNL	: : : : : : : : : : :						
m953	RDGKIDITIPIANLQSGSQHFTDHLKSADIFDAAQYPDIRFVSTKFNFNGKKLVSVDGNL	: : : : : : : : : : :	70	80	90	100	110	120
a953.pep	130	140	150	160	170	180		
	TMHGKTAPVKLKAEKFNQYQSPMLKTEVCGGDFSTTIDRTKWGMMDYLNVGMTKSVRID	: : : : : : : : : : :						
m953	TMHGKTAPVKLKAEKFNQYQSPMEKTEVCGGDFSTTIDRTKWGMMDYLNVGMTKSVRID	: : : : : : : : : : :	130	140	150	160	170	180
a953.pep	QIEAAKQX							
m953	QIEAAKQX							

g954.seq not found yet

g954.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2921>:
m954 seq

1	ATGAAAAAGT	TTTATTTTGT	GCTGCTGGCG	TTGGGTTTGG	CAGCGTGTGG
51	GCAAGAACAA	TCGCAGAAAG	CTGATGCGGA	GCAGTATT	TTTGCCAATA
101	AATATCAATT	TGCAGATGAG	AAACAGGCTT	TTTATTTTGA	ACGCCGCC
151	CGTTCCGTG	TATTGCAACA	AGGCCTTGGC	GGGGATTTG	AGAGGTTT
201	AAAAGGAGAA	ATACCTAATC	AAGAAAATCT	TGCAAAGTAT	CGTAAAATA
251	TTACTCAAGC	AGTCGCTTAT	TATGCGGACA	CGAATGGAGA	TGATGACCCA
301	TACCGCGCT	GCACAAACAGC	TGCGCAAGAT	CGAGAAATCC	TGATGAAGAG
351	TATGTTAAC	AGCGGTGGAG	GCGGTACAAC	TGATTTAGAT	AAGGAAAGTT
401	ATCAAAATT	CCGAAATTCA	ATGCAAGAAT	CCCGTAAAC	AATAACGGAA
451	GCTGAAGCCA	ATTTGCCGAA	AAAATAA		

This corresponds to the amino acid sequence <SEQ ID 2922; ORF 954>:
~~m954_pcr~~

m954.pep

```

1 MKKFYFVLLA LGLAACGQEQ SQKADAEQYF FANKYQFADE KQAFYFERAA
51 RFRVLQQGLG GDFERFLKG IPNQENLAKY RENITQAVAY YADTNGDDDP
101 YRVCKQAAQD AEILMKSMTV SGGGGTTDLD KESYQNYRKS MQECRKTTIE
151 AEANLPKK*

```

a954.seq not found yet

a954.pep not found yet

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2923>:

g957.seq (partial)

```

1 ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTTG CACTTGTATT
51 TGCCTTTGG CTGGGAACAG GTATTGCCA TGAGATTAAT CCGCGTTGGT
101 TTTGAGCGA TACGGCAACT GAAGTACCTG AAAATCCGAA TGCTTTGTG
151 CGCAAACCTG CCCGCGTGT CCGAAATGCC GACAGGGCGG TTGTACATCGT
201 GAAGGAATCG ATGAGGACGG AGGAAAGCCT TGCCGGAGCT GTGGATGACG
251 GTCCGTTGCA GTCCGAGAAG GATTATCTCG CGCTCGCTAT CCGGCTCAGT
301 CGTTGAAAG AAAAGGCCAA ATGGTTTCAC GTAACGGAGC AGGAACATGG
351 GGAAGAGGTT TGGCTGGATT ACTATATCGG CGAGGGCGGT TTGGTTGCGG
401 TTTCGCTTTC GCAACGCTCG CCGGAAGCGT TTGTTAATGC CGAATATCTG
451 TATCGGAACG ATCGTCCGTT TTCTGTAAT TGTTACGGCG GAACGGCTCA
501 CGGGAAAAT TATGAAACGA CAGGAGAATA TCGGGTTGTT TGGCAACCGG
551 ACGGTTCGGT ATTTGATGCG GCGGGGCGCG GGAAATCGG GGAAGATGTT
601 TATGAGCATT GCCTCGGGTG TTATCAGATG GCCCAGGTAT ATTTGGCGAA
651 ATACCGGGAT GTCGCGAATG ACGAGCAGAA GGTTTGGGAC TTCCGCGAAG
701 AGAGCAACCG GATTGCATCG GACTCGCGCG ATTATGTGTT TTATCAGAAT
751 ATGCGGAAAT TGATGCCCG GGGGATgaaG gcaaacagtc ttgttgtcgg
801 ctatgatgcg gacggtCtgc CgcaAAAagt ctattggagt gtcgacaatg
851 gaaaaaaaaacc ccaaagtgtc gaatattatt tggaaaaacgg aaatctttt
901 attgccccat cttcgacggt aaccttggaaa acggatggcg taacggcgga
951 tatgcaaacc tatcatgcgc aacaaacgtt gtatttggat ggg...

```

This corresponds to the amino acid sequence <SEQ ID 2924; ORF 957.ng>:

g957.pep (partial)

```

1 MFKKFKPVLL SFFALVFAFW LGTGIAYEIN PRWFLSDTAT EVPENPNNAFV
51 AKLARLFRNA DRAVVIVKES MRTEESLAGA VDDGPLQSEK DYLALAIRLS
101 RLKEKAKWFH VTEQEHGEEV WLDYYIGEGG LVAVSLSQRS PEAfvNAEYL
151 YRNDRPFSVN VYGGTAHGEN YETTGEYRVV WQPDGSVFDA AGRGKIGEDV
201 YEHLGCYQM AQVYLAKYRD VANDEQKVWD FREESNRRIAS DSRDYVFYQN
251 MRELMRPGRMK ANSLVVGYDA DGLPKVYWS VDNGKKPQSV EYVLKNGNLF
301 IAQSSTVTLK TDGVADMQT YHAQQTLYLD G...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2925>:

m957.seq

```

1 ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTTG CACTTGTATT
51 TGCCTTTGG CTGGGAACAG GTATTGCCA TGAGATTAAT CCGCGTTGGT
101 TTTGAGCGA TACGGCAACT GAAGTACCTG AAAATCCGAA TGCTTTGTG
151 CGCAAACCTG CCCGCGTGT CCGAAATGCC GACAGGGCGG TTGTACATCGT
201 GAAGGAATCG ATAAGGACGG AGGAAATCT TGCCGGAACT GTGGATGACG
251 GTCCGTTGCA GTCCGAGAAG GATTATCTCG CGCTCGCTAT CCGGCTCAGT
301 CGTTGAAAG AAAAGGCCAA ATGGTTTCAC GTAACGGAGC AGGAACATGG
351 GAAAGAGGTT TGGCTGGATT ACCATATCGG CGAGGGCGGT TTGGTTGCGG
401 TTTCGCTTTC GCAACGCTCG CCGGAAGCAT TTGTTAATGC CGAATATCTG
451 TATCGGAACG ATCGTCCGTT TTCTGTAAT TGTTACGGCG GAACGGTTCA
501 CGGGAAAAT TATGAAACGA CAGGAGAATA TCGGGTTGTT TGGCAACCGAG
551 ACGGTTCGGT ATTTGATGCG GCGGGGCGCG GGAAATCGG GGAAGATGTT
601 TATGAGCATT GCCTCGGGTG TTATCAGATG GCCCAGGTAT ATTTGGCGAA
651 ATACCGGGAT GTCGCGAATG ACGAGCAGAA GGTTTGGGAC TTCCGCGAAG
701 AGAGCAACCG AATTGCGCTCG GACTCGCGCA ATTCTGTGTT TTATCAGAAT
751 ATGCGGAAAT TGATGCCCG AGGGATGAAG CGAACACAGTC TTGTGGTCGG
801 CTATGATGCG GACGGCTGCG CGCAAAAAGT CTATTGGAGT TTCGACAATG
851 GAAAAAAACG CCAGACTTC GAATATTATT Tggaaaaacgg AAATCTTTT
901 ATTGCACAAT CTTGCGACGGT AGCATGAAA CGCGATGGCG TAACGGCGGA
951 TATCGAGACC TATCATGCGC AACAGACGTG GTATTTGGAT GGCGGGCGGA
1001 TTGTCCGCGA AGAGAAACAG GGAGACAGAC TGCTGTGTT TCCCTTGAAAC
1051 TTGGAAAATT TGGAAAAAGA GGTGCGCCGT TATGCAAGAGG CTGCGGGAG
1101 ACGTTCGGGC GGCAGGGCGCG ACCTTCTCA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 2926; ORF 957>:

m957.pep

```

1 MFKKFKPVLL SFFALVFAFW LGTGIAYEIN PRWFLSDTAT EVPKNPNNAFV
51 AKLARLFRNA DRAVVIVKES IRTEENLAGT VDDGPLQSEK DYLALAIRLS
101 RLKEKAKWFH VTEQEHGKEV WLDYHIGEGG LVAVSLSQRS PEAfvNAEYL
151 YRNDRPFSVN VYGGTVHGEN YETTGEYRVV WQPDGSVFDA AGRGKIGEDV
201 YEHLGCYQM AQVYLAKYRD VANDEQKVWD FRKESNRRIAS DSRNSVFYQN

```

251 MRELMRGMK ANSLVVGYDA DGLPKVYWS FDNGKKRQSF EYYLKNGLF
 301 IAQSSTVALK ADGVTADMQT YHAQQTWYLD GGRIVREEKQ GDRLPDFPLN
 351 LENLEKEVRR YAEEAARRSG GRRDLSH*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 957 shows 95.2% identity over a 331 aa overlap with a predicted ORF (ORF 957) from *N. gonorrhoeae*

g957/m957 95.2% identity in 331 aa overlap

g957.pep	10	20	30	40	50	60
	MFKKFKPVLLSFFALVFAFWLGTGIAYEINPRWFLSDTATEVPENPNAFVAKLARLFRNA					
m957	MFKKFKPVLLSFFALVFAFWLGTGIAYEINPRWFLSDTATEVPKPNPNAFVAKLARLFRNA					
	10	20	30.	40	50	60
g957.pep	70	80	90	100	110	120
	DRAVVIVKESMRTEESLAGAVDDGPLQSEKDYLALAIRSLRLKEAKWFHVTEQEHGEEV					
m957	DRAVVIVKESIRTEENLAGTVDDGPLQSEKDYLALAIRSLRLKEAKWFHVTEQEHGKEV					
	70	80	90	100	110	120
g957.pep	130	140	150	160	170	180
	WLDYYIGEGGLVAVSLSQRSPEAFVNAEYLYRNDRPFSVNYYGGTAHGENYETTGEYRVV					
m957	WLDYHIGEGGLVAVSLSQRSPEAFVNAEYLYRNDRPFSVNYYGGTVHGENYETTGEYRVV					
	130	140	150	160	170	180
g957.pep	190	200	210	220	230	240
	WQPDGSVFDAAGRKGKIGEDVYEHCLGCYQMAQVYLAKYRDVANDEQKVWDFREESNRIAS					
m957	WQPDGSVFDAAGRKGKIGEDVYEHCLGCYQMAQVYLAKYRDVANDEQKVWDFRKESNRIAS					
	190	200	210	220	230	240
g957.pep	250	260	270	280	290	300
	DSRDYVFYQNMRELMRGMKANSVVGYDADGLPQKVYWSVDNGKKPQSVEYYLKNGLF	:				
m957	DSRNSVFYQNMRELMRGMKANSVVGYDADGLPQKVYWSFDNGKKRQSFSEYYLKNGLF	250	260	270	280	290
	250	260	270	280	290	300
g957.pep	310	320	330			
	IAQSSTVTLKTDGVADMQTYHAQQTLYLDG					
m957	IAQSSTVALKADGVTADMQTYHAQQTWYLDGGRIVREEKQGDRLPDFPLNLENLEKEVRR	310	320	330	340	350
	310	320	330	340	350	360
m957	YAEEAARRRSRGGRDLSHX	370				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2927>:
 a957.seq

```

 1 ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTTG CACTTGTATT
 51 TGCCTTTTGG CTGGGAACGG GTATTGCCATA TGAGATTAAT CCGCGTTGGT
 101 TTTGAGCGA TACGGCAACT GAAAATCCGA ATGCTTTGT GGCAGAACTT
 151 GCCCGCTGT TCCGAAATGC CGACAGGGCG GTTGTCACTCG TGAAGGAATC
 201 GATGAGGACG GAGGAAAGTC TTGCGGGAGC TTGCGATGAC GGTCCGTTGC
 251 AGTCGGAGAA GGATTATCTT GCACTCGCTG TCCGGCTCATCG TCGTTTGAAA
 301 GAAAAGCCGA AATGGTTCA CGTAACGGAG CAGGAACATG GGGAAAGAGGT
 351 TTGGCTGGAT TACTATATCG CGGAGGGCGG TTTGGTTGCG GTTTCGCTTT
 401 CGCAACGCTC GCGGGAAAGCG TTTGTTAATG CCGAATATCT GTATCGGAAC
 451 GATCGTCCGT TTTCTGTAAA TGTGTACGGC GGAACGGTTG ACGGGGAAAAA
 501 TTATGAAACG ACAGGGAGAT ATCGGGTTGT TTGGCAACCG GACGGTTCGG
 551 TATTTGATGC GTCGGGGCGC GGGAAAATCG GGGAAAGATGT TTATGAGCAT
 601 TGCCCTCGGGT GTTATCAGAT GGCCCAGGTA TATTGCGCGA AATATCGGG
 651 TGTGCGGAAT GATGAGCAGA AGGTTGGGA CTTCGCGCAA GAGAGTAACC
 701 GGATTGCGTC GGACTCGGGC GATTCTGTG TTTATCAGAA TATGCGGGAA
 751 TTGATGCCCG GAGGGATGAA GGCAAAACAGT CTTGTGGTCG GCTATGATGC
 801 GGACGGTCTG CCGCAGAAAG TCTATTGGAG TTTGACAAT GGGAAAAAAC
 851 GCCAGAGTTT CGAAATTAT TTGAAAACAG GAAATCTTT TATTGACCAA
 901 TCTTCGACGG TAGCATTGAA AGCGGATGGC GTAACGGCGG ATATGCAGAC

```

951 CTATCATGCCG CAACAGACGT GGTATTTAGA TGGCGGGCGG ATTGTCCCGC
 1001 AAGAGAAAACA GGGGGACAGA CTGCCTGATT TTCCCTTGAA CTTGGAAGAT
 1051 TTGGAAAAAG AGGTGAGCCG TTATGCAGAG GCTGCGGCAGA GACGTTGGGG
 1101 CGGCAGGCCG GACCTTCTC ACTGA

This corresponds to the amino acid sequence <SEQ ID 2928; ORF 957.a>:

a957.pep

```

 1  MFKKFKPVLL SFFALVFAFW LGTGIAYEIN PRWFLSDTAT ENPNAFVAKL
 51  ARLFRNADRA VVIVKESMRT EESLAGAVDD GPLQSEKDYL ALAVRLSRLK
 101 EKAKWFHVTE QEHEEEVWLD YYIGEGGLVA VSLSQRSPEA FVNAEYLYRN
 151 DRPF SVN VY GTVHGENYET TGEYRVVWQP DGSVFDASGR GKIGEDVYEH
 201 CLGCYQMAQV YLAKYRDVAN DEQKVWDFRE ESNRRIASDSR DSVFYQNMRE
 251 LMPRGMKANS LVVGYDADGL PQKVYWSFDN GKKRQSFEYY LKNGNLFIAQ
 301 SSSTVALKADG VTADMQTYHA QQTWYLDGGR IVREEKQGDR LPDFPLNLED
 351 LEKEVSR YAEAAARRSGGRRDL SHX
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 957 shows 96.3% identity over a 377 aa overlap with a predicted ORF (ORF 957) from *N. meningitidis*

a957/m957 96.3% identity in 377 aa overlap

a957.pep	10	20	30	40	50	
	MFKKFKPVLLSFFALVFAFWLGTGIAYEINPRWFLSDTATE---					NPNAFVAKLARLFRNA
m957						
	MFKKFKPVLLSFFALVFAFWLGTGIAYEINPRWFLSDTATEVPKNPNAFVAKLARLFRNA					
	10	20	30	40	50	60
a957.pep	60	70	80	90	100	110
	DRAVVIVKESMRTEESLAGAVDDGPLQSEKDYLALAVRLSRLKEKAKWFHVTEQEHEEV					
m957						
	DRAVVIVKESIRTEENLAGTVDDGPLQSEKDYLALAIRLSRLKEKAKWFHVTEQEHGKEV					
	70	80	90	100	110	120
a957.pep	120	130	140	150	160	170
	WLDYYIGEGGLVAVSLSQRSPEAFVNAEYLYRNDRPF SVNVYGGTVHGENYETTGEYRVV					
m957						
	WLDYHIGEGGLVAVSLSQRSPEAFVNAEYLYRNDRPF SVNVYGGTVHGENYETTGEYRVV					
	130	140	150	160	170	180
a957.pep	180	190	200	210	220	230
	WQPDGSVFDASGRKIGEDVYEHCLGYQMAQVYLAKYRDVANDEQKVWDFREESNRIAS					
m957						
	WQPDGSVFDAAAGRKIGEDVYEHCLGYQMAQVYLAKYRDVANDEQKVWDFRKESNRIAS					
	190	200	210	220	230	240
a957.pep	240	250	260	270	280	290
	DSRDSVYQNMRELMPRGMKANSLVVGYDADGLPQKVYWSFDNGKKRQSFEYYLKNGNLF					
m957						
	DSRNSVYQNMRELMPRGMKANSLVVGYDADGLPQKVYWSFDNGKKRQSFEYYLKNGNLF					
	250	260	270	280	290	300
a957.pep	300	310	320	330	340	350
	IAQSSTVALKADGV TADMQTYHAQQTWYLDGGRIVREEKQGDRLPDFPLNLEDLEKEVSR					
m957						
	IAQSSTVALKADGV TADMQTYHAQQTWYLDGGRIVREEKQGDRLPDFPLNLENLEKEVRR					
	310	320	330	340	350	360
a957.pep	360	370				
	YAEAAARRSGGRRDL SHX					
m957						
	YAEAAARRSGGRRDL SHX					
	370					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2929>:

g958.seq

```

 1  TTGGCTCGTT TATTTCACT CAAACCAC TGCTGGCAT TGGGCTTCTG
 51  TTTCGGCACG CATTGCGCCG CCGATACCGT TGCGCGGGAA GAGGCAGGACG
```

101 GGC GTG TCGC AGA AGG CGGT GCG CAG GGG CG CGT CGG AATC CGC ACA AAG CT
 151 TCC GATT TGA CCCT CGG TT GAC CTG CCTG TTT TG CAG TA ACG AAAG CGG
 201 CAG CCC CGAG AGA ACC GAAG CGG CGT CA AGG CAG CGG GC GAAG CAT CCG
 251 TCCC CGA AGA CT ATAC CGC ATT GTT GCG AC AGG ATG GA AGG AC AGT CG
 301 AAG GTT AAGG TG CGC GCG GA AGG AAG CGT T ATCAT CGA AC GGG AC GGC GCG
 351 AGT CCT CAAT ACC GAT TGG CGG ATT AC GA CGA GT CGG G GAC ACC GT TA
 401 CGG TAC CGA CGG CGT CC CGG CCT CGC CT CCA AC AGG AC CGG TAC CG CT GAT TCG GGG G
 451 GAA ACC CT GA CCT AC AAT CT CG ATC AGC AG ACC CGG CA AG CG CACA AC AGT
 501 CGG TAT GGAA ACC GA ACA AG GCG GAC CGG GCG TGT CAA AGC GTC AG CGG CCA
 551 CGG CG GAA AT GTT GGG GAA GGG CGT TAC A ACT GAC CGG A ACC CA AAT TC
 601 AAC CCT GT T CGG CGG GAGA TG CGG CT GG TAT GT CA AGG CGG CCT CT GGT
 651 CGA AGG CG AT CGG GAA AG CG AT AGG CG T GAT CCA AC AC GCG CTT TCG
 701 TG TT CGG CGG CG CG TT CCT CC TT TT CT ATAC GC CT TGG CGG GA CT TCC CGC TT
 751 GAC GG CA AC CG AAA AG CG CG ACT GCT CG TC CGT CG CG TAT CT CG CG GT TC
 801 GG AC CG CG GT T CCG CCT TCG TCC CT ATT A TT CA AC CCTT GCG CGG CG
 851 TCG AT GCG CA CCC CGC AT TAT CG CGA AC CG CG CG CG GCG AC GCG TT
 901 GAC GG GAC AAA TCC GTT AC CT CGT CG CG AT CAG CG GAC AG ACC GAC CT
 951 GAC CT GG TT CG CG CAC GATA AG AAA AG CG CG AGG A AC ACG CAG
 1001 CAAA AT GGCA GC ACC CGG CA AC GAT TT CG CG AC AG C GT TCA GCG GGG TGT
 1051 GAT TT CA ACC AAG T CT CG CA CAG CGG CT AC TAC CG CG ACT TT AC CGG CG
 1101 CGA AGG AA AT CG CG CG CA AC G TCA AC CT CA CG CG CG CG TA TGG CT GG ATT
 1151 AT CG CG CG CG GGC CG CG GGA GGC AG CG CT GA AT CG CG CG CT TT CG GTT
 1201 AA ATAC CAGA CG CT GG CG AA CCA AG CG CG TAC AA AG AG C G AAC CT TAC
 1251 CAT CAT GCCC CG CTT TT CT CG CG AT TT CG CG CA TAAA AA AG CG CA GGC AGG CG
 1301 AA AT CG CG GT GT CG CG CA AA TTA CC CG CT CG AG CG CA CG CG CG CCA
 1351 GAC CG CG AG CG GACT GT CG GT GT AT CCA AT GG GG AT TT CAG CAA
 1401 CAG CT GG GG TAC CG CG CG CC AA ACT CG CG GCT GC AC CG CC ACT TATT
 1451 GC CT CG AC AG TT CG CG CG CG AA AG CG AT CC CG AG CG GT CG GCG CG TT
 1501 CCC GTT GT CA AT AT CG AC CG CG CG CA ACC CG CA ACC CG CG AT AC CG CG
 1551 GTT CG CG CG CG GG AG CG CG GT CG CG AA ACC AT CG CA CG CG CG CG CG
 1601 AT AT CC TG CCA AT AT CG CA AA CG AC AC CT CG CG CA AT TT CG CG
 1651 AG CAG CT CG GCT CG CG CC GT TT CC CG GCA AA AC AC CT CT ATT AC CG CG
 1701 CG AC CG C AT CG AAC CG CG CA AC AG CG CT TC CAC CG CG GT CG AG CG CG
 1751 TTT GG AC CG CG CG AC CG CG GAG GAG CG GT TT CG CG CG CG TAT CG GT
 1801 AA AT TCT ATT TCA AGG AT GA TG CG GT GAT G CT TG AC CG CG CA GCG CG
 1851 AA AT CC CG CG AG CG CG TT CG CG ACT CG CG GT CG CG AT TG CG CG
 1901 CG CG CG CG TT CAC CT CG AC CG AC AT CG CA AC CA AA AC CG AC
 1951 CG CG CG CG AC AT TA CG
 2001 AGT GTT GA AC GCG CG CT AC AA TA CG CG CG CG CA AC CG AA AA AT CT AC
 2051 AGG CG GAC CG CG TT CG AT TT TAC G AC AA AC TC AG CG CG CT CG AC
 2101 GC AC AA AT CG CG CG CG CG CG CA AC CT GT CT CG CG CG CG
 2151 CG GCG TT GA CG CAA AA AC CG AT AG AA AT CG CG CG GT CG AG AA AT
 2201 AA AG CAG TT CG
 2251 ACC CG CG CG AA CA CCT AC AA AC AC CG CG CG CG CG CG CG CG CG
 2301 AG AC CT CAG C AG CG CG CG CA GAA ACC CG CG CG CG CG CG CG
 2351 TT CG CG CG CT CA TCC CG
 2401 CC CT GA

This corresponds to the amino acid sequence <SEQ ID 2930; ORF 958.ng>:
g958.pep

1 LARL FLS LKPL VL ALG FCF GT HCA ADT VAA E EAD GRV AEGG AQ GASE SA QQA
 51 S DLT LG ST CL FCS N EGS S P E R TE AAV QSG E AS VP EDY TR IV ADR MEG QOS
 101 KV KV RA EG SV II ERD GAV LN TD WAD YD QSG DT VTV GDR FA LQ QDG TL IRG
 151 ET LT YN LD QQ TGE AHN VR ME TE QG GRR LQS VS RTA EML GE GRY KLT ET QF
 201 NT CSAG DAGW YV KA AS VE AD RG KG GI GV AKH AAF VFG GVP LY TPW AD FPL
 251 DGN RKS GLL V PSV SAG SD DV SLS VP YY FNL AP NF DAT FAP GII GER GAT F
 301 DG QI RY LR PD Y SG QT DLT WL PH DK KS GR NN RY QAK WQ HRH DIS DT LQ AGV
 351 DFN QV SD S GY YR DF YG GEE I AGN VN NL RRV WLD YG G RAAG G S L N AGL SV Q
 401 KY QTL AN QSG YK DE PY AIMP RLS ADW HK NA GRA QIG VSA Q FTR FSH DGR Q
 451 DGS RL VV Y PG IK WDF SN SW Y V RPK I GL HA TY YS L DS FGG KAS RSV GRV L
 501 PV VNI DGG TT FER NTR L FGG G VV QTI EPL FYN YI PAK SQ ND LPN FDS SE
 551 SS FG YG QL FR EN LY YG NDR I NA ANS L ST AV QSR IL DG AT G EER FRAG IG Q
 601 KFY FK DDA VM LD GS VG KN PR SR SDW VAF AS G GIG GR F TLD SSI HYN QND K
 651 RAE HYA VG AG YRP A PG KVL N ARY K YG RNE K IYL QAD GS YF YDK L S QLD LS
 701 A QW PLTR NLS A VV RY NY GFE AKK PI EML AG A EY KSS CG CW GAG VYA QRY V
 751 TG E NTY KNA V FFS L QL K DLS S VGR N PAGR M DV A VPG YI PA HSL SAGR NK R
 801 P*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2931>:
m958.seq

1 TT GG CT CG TT TAT TTT CACT CAA ACC ACT G GT GCT GGC AT TGG CG CT CT G
 51 CT CG CG CAC G CATT CGC GCG CG CG CG AT GC CG TGT CG CG GAG GAA AC CG
 101 ACA AT CG CA CG CG CG AG CG TT CG GA CG GT CG CG ACC C AT AC AG

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151 CCTACCAGCC TGAGCCTCGG TTGACACTGC CTGTTTGCA GTAACGAAAG
201 CGGCAGCCCC GAGAGAACCG AAGCCGCCGT CCAAGGCAGC GGCAGAACAT
251 CCATCCCCGA AGACTATACG CGCATTGTT CGACAGGAGT GGAAGGACAG
301 TCGCAGGTGC AGGTGGTGC CGAAGGCAAC GTCGTCGTG AACGCAACCG
351 GACGCCCTAA ATAACCGATT GGGCGGATTA CGACCAAGTCG GGCGACACCG
401 TTACCGCAGG CGACCGCTTC GCCCCTCAAAC AGGACGGTAC GCTGATTCCG
451 GGCAGAACCC TGACCTACAA TCTCGAGCAG CAGACGGGG AAGCGCACAA
501 CGTCCGCATG GAAATCGAAC AAGGCGGACG CGGCGTGCAC AGCGTCAGCC
551 GCACCCCGA AATGTTGGC GAAGGGCATT ACAAACTGAC GGAAACCCAA
601 TTCAACACCT GTTCCGGGG CGATGCCGGC TGGTATGTCA AGGCAGCCTC
651 TGTGCAAGGC GATCGGGAAA AAGGCATAGG CGTTGCCAAA CACGCCGCT
701 TCGTGTTCGG CGGGCTTCCC ATTTCCTACA CCCCTGGGC GGACTTCCCG
751 CTTGACGGCA ACCGAAAG CGGCGTGCCT GTTCCCTCAC TGTCCGCCGG
801 TTCGGACGGC GTTCCCTTT CGGTCCCTA TTATTTCAC ACAGCAGCCCA
851 ATCTCGATGC CACGTCGGC CCCAGCGTGA TCGGCGAACG CGGCAGCGTC
901 TTGACGGGC AGGTACGCTA CCTGCGGGCG GATTATGCCG GCCAGTCGA
951 CCTGACCTGG CTGGCGACG ACAAGAAAAG CGGCAGGAAT AACCGCTATC
1001 AGGCCAAATG GCACCATCGG CACGACATTG CGGACACGCT TCAGGGGGT
1051 GTCGATTCA ACCAAGTCTC CGACAGCGGC TACTACCGC ACTTTTACGG
1101 CAACAAAGAA ATGCCGGCA ACGTCAACCT CAACCGCCGT GTATGGCTGG
1151 ATTATGGCG CAGGGCGGC GGCGCAGCC TGAAATGCCG CCTTTGGTT
1201 CTGAAATACC AGACGCTGGC AAACCAAAGG CGCTACAAAG ACAAAACCGTA
1251 TGCCCTCATG CGGGCGCTT CGGTCGAGTG CGGTTAAAAC ACCGGCGAGGG
1301 CGCAAATCGG CGTGTCCGCA CAATTACCC GATTCAAGCCA CGACAGCCGC
1351 CAAGACGGCA GCCGCCTGGT CGTCTATCCC GACATCAAAT GGGATTTCA
1401 CAACAGCTGG GGCTATGTCC GTCCCAAAC CGGACTGCAC GCCACCTATT
1451 ACAGCCTCAA CGGCTTCGGC AGCCAAGAAC CGGCAGCGCT CAGCCGCACT
1501 CTGCCATTG TCAACATCGA CAGGGCGCA ACTTTTGAGC GGAATACCGC
1551 GATGTTCGGC GGAGAAAGTCC TGCAACCCCT CGAGCGCGC CTGTTCTACA
1601 ACTATATTCC TGCCAAATCC CAAAAGGACC TGCCCAAATT CGATTGTCG
1651 GAAAGCAGCT TCAGGCTACGG GCAGCTCTT CGCGAAAACC TCTATTACGG
1701 CAACGACAGG ATTAACACCG CAAACAGCCT TTCCGCGGCC GTGCAAAGCC
1751 GTATTTGGA CGGCGCGACG GGGGAAGAGC GTTCCCGCFC CGGCATCGGT
1801 CAGAAATTCT ATTTCAAGGA TGATGCGGTG ATGCTTGACG GCAGCGTCGG
1851 CAAAAAAACCG CGCAACCGTT CCGACTGGGT GGCAATTGCC TCCGGCAGCA
1901 TCGGCAGCCG CTTCATCTC GACAGCAGCA TCCACTACAA CCAAAACGAC
1951 AAACGCGCCG AGAAACTACGC CGTCCGTGCA AGCTACCGC CCGCACAGGG
2001 CAAAGTGCTG AACGCGCCGT ACAAAATACGG CGCAGAACGAA AAAATCTACC
2051 TGAAGTCCGA CGGTTCTAT TTTCACGACA AACTCAGCCA GCTCGACCTG
2101 TCCGCACAAT GGCGCTGAC GCGCAACCTG TCGGCGTCG TCCGTTACAA
2151 CTACGGTTTT GAAGCCAAAA AACCGATAGA GGTGCTGGCG GGTGCGGAAT
2201 ACAAAAGCAG TTGCGGGTGC TGCGGGCGG GCGTGTACGC CCAACGCTAC
2251 GTTACCGGGC AAAAACACCTA CAAAAAACCGT GTCTTTTCT CACTTCAGTT
2301 GAAAGACCTC AGCAGTGTG GCAGAACCC CGCAGACAGG ATGGATGTGCG
2351 CGGTTCCGG CTATATCACC GCCCACTCTC TTTCGCGCCG ACGCAACAAA
2401 CGACCCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2932; ORF 958>:

m958.pep

```

1 LARLFSLKPL VLALGLCFGT HCAAADAVAA EETDNPTAGE SVRSVSEPIQ
51 PTSLSLGSTC LFCSNESGSP ERTEAAVQGS GEASIPEDYT RIVADRMEQ
101 SQVQVRAEGN VVVERNRTTL NTDWADYDQS GDTVTAGDRF ALQQDGTLLR
151 GETLTYNLEQ QTGEAHNVRM EIEQGGRRLQ SVSRTAEMLG EGHYKLTEQ
201 FNTCSAGDAG WYVKAASVEA DREKGIGVAK HAAFVFGGVP IFYTPWADFP
251 LDGNRKSGLL VPSLSAGSDG VSLSPVYYFN LAPNLDATFA PSVIGERGAV
301 FDGQVGYRLP DYAGQSDLTW LPHDKKSGRN NRYQAKWQHR HDISDTRLQAG
351 VDFNQVPSDG YYRDFYGNKE IAGNVNLNRV WLWDYGGRAA GGSLNAGLSV
401 LKYQTLANQS GYKDCKPYALM PRLSVEWRKN TGRAQICGVSA QFTRFSHDSR
451 QDGSRVVYP DIKWDFNSW GYVRPKLGLH ATYYSLNRFQ SQEARRVSRT
501 LPIVNIDSGA TFERNTRMFG GEVLQTLERPV LFYNYIPAKS QNDLPNFDS
551 ESSFGYQQLF RENLYYGNLD INTANSLSAA VQSRILDGAT GEERFRAGIG
601 QKFYFKDDAV MLDGSVGKKP RNRSWDWVAFA SGSIGSRFIL DSSIHYNQND
651 KRAENYAVGA SYRPAQGKVL NARYKYGRNE KIYLKSDGSY FYDKLSQLDL
701 SAQWPPLTRNL SAVVRYNYGF EAKKPIEVLA GAEYKSSCGC WGAGVYAQRY
751 VTGENTYKNA VFFSLQLKDL SSVGRNPADR MDVAVPGYIT AHSLASGRNK
801 RP*

```

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

ORF 958 shows 89.3% identity over a 802 aa overlap with a predicted ORF (ORF 958) from *N. gonorrhoeae*

m958/g958 89.3% identity in 802 aa overlap

	10	20	30	40	50	60
m958.pep	LARLFSLKPLVLALGLCFGTHCAAADAVAAEETDNPTAGESVRSVSEPIQPTSLISLGSTC					
g958	LARLFSLKPLVLALGFCFGTHCAA-DTVAEEADGRVAEGGAQGASESAQASDLTLGSTC	10	20	30	40	50
		70	80	90	100	110
m958.pep	LFCSNESGSPERTEAAVQGSGEASIPEDYTRIVADRMEGQSQVQVRAEGNVVVERNRTL					120
g958	LFCSNESGSPERTEAAVQGSGEASVPEDYTRIVADRMEGQSQVKVRAEGSVIIERDGA	60	70	80	90	100
		130	140	150	160	170
m958.pep	NTDWADYDQSGDTVTAGDRFALQQDGTЛИRGETLTYNLEQQTGEAHNVRMIEQGGRLQ					180
g958	NTDWADYDQSGDTVTAGDRFALQQDGTЛИRGETLTYNLDQQTGEAHNVRMETEQGGRLQ	120	130	140	150	160
		190	200	210	220	230
m958.pep	SVSRTAEMLGEGHYKLTELQFTCSAGDAGWVKAASVEADREKGIGVAKHAAFVFGGP					240
g958	SVSRTAEMLGEGRYKLTELQFTCSAGDAGWVKAASVEADRGKGIGVAKHAAFVFGGP	180	190	200	210	220
		250	260	270	280	290
m958.pep	IFYTPWADFPLDGNRKSGLLVPSLSAGSDGVSLSPVYYFNLPNLATFAPSVIGERAV					300
g958	LFYTPWADFPLDGNRKSGLLVPSVSAGSDGVSLSPVYYFNLPNLATFAPGIIGERAT	240	250	260	270	280
		310	320	330	340	350
m958.pep	FDGQVRYLRPDYAGQSDLTLWPHDKSGRNRRYQAKWQHRHDISDTLQAGVDFNQVSDSG					360
g958	FDGQIRYLRPDYSGQTDLTWPHDKSGRNRRYQAKWQHRHDISDTLQAGVDFNQVSDSG	300	310	320	330	340
		370	380	390	400	410
m958.pep	YYRDFYGNKEIAGVNVLNRRLWLDYGGRAAGGSLNAGLSVLKYQTLANQSGYKDPKYALM					420
g958	YYRDFYGGEEIAGVNVLNRRLWLDYGGRAAGGSLNAGLSVQKYQTLANQSGYKDPEYAIM	360	370	380	390	400
		430	440	450	460	470
m958.pep	PRLSVEWRKNTGRAQIGVSAQFTRFSHDSRQDGSRLLVYVDPIDKWDFTNSWGYVRPKLGLH					480
g958	PRLSADWHKNAGRAQIGVSAQFTRFSHDRQDGSRLLVYVPGIKWDFTSNSWGYVRPKLGLH	420	430	440	450	460
		490	500	510	520	530
m958.pep	ATYYSLNRFGSQEARRVSRTLPIVNIIDSGATFERNTRMFGGEVLQTEPRLFYNYIPAKS					540
g958	ATYYSLDSFGGKASRSVGRVLPVVNIIDGGTFERNTRLFGGGVVQTEPRLFYNYIPAKS	480	490	500	510	520
		550	560	570	580	590
m958.pep	QNDLPNFDSSSESSFGYQQLFRENLYYGNDRINTANSLSAAVQSRILDGATGEERFRAGIG					600
g958	QNDLPNFDSSSESSFGYQQLFRENLYYGNDRINAANSLSTAVQSRILDGATGEERFRAGIG	540	550	560	570	580
		610	620	630	640	650
m958.pep	OKFYFKDDAVMLDGSVGKKPRNRSDWVAFASGSIGSRFIELDSSIHYNQNDKRAENYAVGA					660
g958	OKFYFKDDAVMLDGSVGKNPRSRSDWVAFASGGIGGRFLDSSIHYNQNDKRAEHYAVGA	600	610	620	630	640
		670	680	690	700	710
m958.pep	SYRPAQGVNLNARYKYGRNEKIYLKSDGSFYDKLSQDLSAQWPLTRNLSAVVRYNYGF					720
g958	GYRPAPGVNLNARYKYGRNEKIYLQADGSFYDKLSQDLSAQWPLTRNLSAVVRYNYGF	660	670	680	690	700
		710				

	730	740	750	760	770	780
m958.pep	EAKKPIEVLAGAEYKSSCGCWAGVYAQRYVTGENTYKNAVFFSLQLKDLSVGRNPADR					
g958	: : : : : : : : : EAKKPIEMLAGAEYKSSCGCWAGVYAQRYVTGENTYKNAVFFSLQLKDLSVGRNPAGR					
	720	730	740	750	760	770
	790	800				
m958.pep	MDVAVPGYITAHSLSGRNKRP					
g958	: : MDVAVPGYIPAHSLSAGRNKRPX					
	780	790	800			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2933>:

a958.seq

```

1   TTGGCTCGTT TATTTTCACT CAAACCACTG GTGCTGGCAT TGGGCTTCTG
51  TTTGGCAGC CATTGCGCCG CCGCCGATGC CGTTGCGGGC GAGGAAACGG
101 ACAATCCGAC CGCCGGAGGA AGCGTTCGGA CGGTGTCCGA ACCCATACAG
151 CCTACCAGCC TGAGCCTCGG TTCGACCTGC CTGTTTGCA GTAACGAAAG
201 CGGCAGCCCC GAGAGAACCG AAGCCGCCGT CCAAGGCAGC GCGAAGACAT
251 CCATCCCCGA AGACTATACG CGCATTGTTG CCGACAGGAT GGAAGGACAG
301 TCGCAGGTGC AGGTCGCTGC CGAAGGCAAC GTCGCTGTCG AACGCAATCG
351 GACGACCCCTC AATGGCGATT GGGGGATTAA CGACCACTCG GGCACACCCG
401 TTACCGCAGG CGACCGGTT GCCCTCCAAC AGGACGGTAC GCTGATTCCG
451 GGCAGAACCC TGACCTACAA TCTCGAGCAG CAGACCGGGG AAGCCGACAA
501 CGTCCGTATG GAAACCGAAC ACGGCGGACG GCGGCTGCAA AGCGTCAGCC
551 GCACCGCCGA AATGTTGGC GAAGGGATTAA CAAACTGAC GGAAACCCAA
601 TTCAACACCT GTTCCGCGGG CGATGCCGGC TGGTATGTCA AGGCCGCTTC
651 CGTCGAAGCC GATGGGGAAA AAGGCATAAGG CGTTGCCAAA CACGCCGCT
701 TCGTGTTCGG CGGCCTTCCC ATTTTCTACA CCCCTTGGGC GGACTTCCCG
751 CTTGACGGCA ACCGCAAAAG CGGCCTGCTC GTTCCCTCAC TGTCCGCCGG
801 TTCGGAGGGC GTTCCCTTCTT CGGTTCCCTA TTATTTCAAC CTTGCCCCA
851 ATCTCGATGC CACGTTCGCG CCCGGCGTGA TCGCGAACCG CGGCACGGTC
901 TTTGACGGGC AGGTACGCTA CCTGCGGCCG GATTATGCCG GCGAGTCCGA
951 CCTGACCTGG CTGCGCACG ACAAGAAAAG CGGCAGGAAT AACCGCTATC
1001 AGGCAGAAATG GCAGCACCGG CACGACATTG CCGACACGCT TCAGGCGGGT
1051 GTCGATTTCA ACCAAGTCTC CGACAGCGGC TACTACCGC ACTTTTACGG
1101 CAACAAAGAA ATCGCCGGCA ACGTCAACCT CAACCGCCGT GTATGGCTGG
1151 ATTATGGCGG CAGGGCGGGC GGCGCAGCC TGATGCCGG CCTTTCGGTT
1201 CTGAAATACC AGACGCTGGC AAACCAAAGC GGCTACAAAG ACAAACCGTA
1251 TGCCCTGATG CCGCGCTTT CCGCCGATTG GCGCAAAAC ACCGGCAGGG
1301 CGCAAATCGG CGTGTCCGCC CAATTACCC GCTTCAGCCA CGACAGCCGC
1351 CAAGACGGCA GCGCCCTCGT CGTCTATCCC GACATCAAAT GGGATTTTAG
1401 CAACAGCTGG GTTACGTCC GTCCCAAACT CGGACTGCA CGCACCTATT
1451 ACAGCCTAA CCGCTTCCGG AGCCAAGAAG CCCGACGCCT CAGCCGCACT
1501 CTGCCCATCG TCAACATCGA CAGCGGCATG ACCTTCGAAC GCAATACGG
1551 GATGTTCGGC GGCAGGAGTC TGCAAACCT CGAGCCGCGC CTGTTCTACA
1601 ACTATATTCC TGCCAAATCC CAAACACGACC TGCCCAATT CGATTGTCG
1651 GAAAGCAGCT TCGGCTACGG CGACGTTTTT CGTGAACCG TCTATTACGG
1701 CAACGACAGG ATTAACACCG CAAACAGCT TTCCGCCGCC GTGCAAAGCC
1751 GTATTTTGGG CGCGCGACG GGGGAAGAGC GTTCCGCCGCC CGGCATCGGG
1801 CAGAAATTCT ACTTCAAAAA CGACGCGATC ATGCTTGACG GCAGTGTGG
1851 CAAACAAACCG CGCAGCGCTT CGGACTGGGT GGCATTCCGCC TCCAGCGGCA
1901 TCGGCAGGCC CTTCATCTC GACAGCAGCA TCCACTACAA CCAAACGAC
1951 AAACGCGCCG AGAAACTACGC CGTCGGTGCAG ACTTACCGTC CGGCACAGGG
2001 CAAAGTCTG AAGCAGCGCT ACAAAATACGG GCGCAACGAA AAAATCTACC
2051 TGAAGTCCGA CGGTTCTAT TTTACGACA AACTCAGCCA GCTCGACCTG
2101 TCCGCAACAT GGCGCTGTCG GCGCAACCTG TCGGCCGTGCG TCCGTTACAA
2151 CTACGGTTT GAAGCCAAA AACCGATAGA GTGCTGCGCG GGTGCGGAAT
2201 ACAAAAAGCAG TTGCGCGTGC TGGGCGCGG GCGTGTACGC CCAACGCTAC
2251 GTTACCGGGC AAAACACCTA CAAAACGCT GTCTTTTCT CACTTCAGTT
2301 GAAAGACCTC AGCAGTGTGCG GCAGAAACCC CGCAGACAGG ATGGATGTCG
2351 CCGTTCCGG CTATATCCCC GCGCACTCTC TTCCGCCGCC ACGCAACAAA
2401 CGGCCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2934; ORF 958.a>:

a958.pep

```

1 LARLFSLKPL VLALGFCTGT HCAAAADAVAA EETDNPTAGG SVRSVSEPIQ
51 PTSLSLGSTC LFCSNESGSP ERTEAAVQGS GEASIPEDYT RIVADRMEGQ
101 SQVQVRAEGN VVVERNRTTL NADWADYDQS GDTVTAGDRF ALQQDGTLLR
151 GETLTYNLEQ QTGEAHNVRM ETEHGGRRHQ SVSRTAEMLG EGHYKLTTETQ
201 FNTCSAGDAG WYVKAASVEA DREKGIGVAK HAAVFVFGGPV IFYTPWADFP

```

251 LDG NRKSGLL VPSLSAGSDG VSLSVPYYFN LAPNLDATFA PGVIGERGAV
 301 FDGQVRYLRP DYAGQSDLTW LPHDKSGRN NRYQAKWQHR HDISDTLQAG
 351 VDFNQVSDSG YYRDFYGNKE IAGNVNLNRR VLWDYGGRAA GGSLNAGLSV
 401 LKYQTLANQS GYKDCKPYALM PRLSADWRKN TGRAQIGVSA QFTRFSHDSR
 451 QDGSRLVVYP DIKWDFNSW GYVRPKLGLH ATYYSLNRFQ SQEARRVSRT
 501 LPIVNIDSGM TFERNTRMFG GGVLQTLLEPR LFYNYIPAKS QNDLPNFDS
 551 ESSFGYQGLF RENLYYYGNDR INTANSLSAA VQSRILDGAT GEERFRAGIG
 601 QKFYFKNDAV MLDGSVGKKP RSRSDWVAFA SSGIGSRFIL DSSIHYNQND
 651 KRAENYAVGA SYRPAQGKVL NARYKYGRNE KIYLKSDGSY FYDKLSQLDL
 701 SAQWPPLTRNL SAVVRYNYGF EAKKPIEVLA GAEYKSSCGC WGAGVYAQR
 751 VTGENTYKNA VFFSLQLKDL SSVGRNPADR MDVAVPGYIP AHSLSGRNL
 801 RP*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 957 shows 96.3% identity over a 377 aa overlap with a predicted ORF (ORF 957) from *N. meningitidis*

a958/m958 98.1% identity in 802 aa overlap

a958.pep	10	20	30	40	50	60
	LARLFSLKPLVLALGFCFGTHCAAADAVAAEETDNPTAGGSVRSVSEPIQPTSLSLGSTC					
m958	LARLFSLKPLVLALGLCFGTHCAAADAVAAEETDNPTAGESVRSVSEPIQPTSLSLGSTC					
	10	20	30	40	50	60
a958.pep	70	80	90	100	110	120
	LFCSNESGSPERTEAAVQGSGEASIPEDYTRIVADMEGQSQVQVRAEGNVVVERNRTTL					
m958	LFCSNESGSPERTEAAVQGSGEASIPEDYTRIVADMEGQSQVQVRAEGNVVVERNRTTL					
	70	80	90	100	110	120
a958.pep	130	140	150	160	170	180
	NADWADYDQSGDTVTAGDRFALQQDGTLLIRGETLTYNLEQQTGEAHNVRMETEHGGRRQ	:				
m958	NTDWADYDQSGDTVTAGDRFALQQDGTLLIRGETLTYNLEQQTGEAHNVRMETEQGGRRQ					
	130	140	150	160	170	180
a958.pep	190	200	210	220	230	240
	SVSRTAEMLGEGHYKLTELQFNTCSAGDAGWVYVKAASVEADREKGIGVAKHAASFVFGGP					
m958	SVSRTAEMLGEGHYKLTELQFNTCSAGDAGWVYVKAASVEADREKGIGVAKHAASFVFGGP					
	190	200	210	220	230	240
a958.pep	250	260	270	280	290	300
	IFYTPWADFPLDGNRKSGLLVPISLAGSDGVSLSPVYYFN LAPNLDATFAPGVIGERGAV					
m958	IFYTPWADFPLDGNRKSGLLVPISLAGSDGVSLSPVYYFN LAPNLDATFAPSVIGERGAV					
	250	260	270	280	290	300
a958.pep	310	320	330	340	350	360
	FDGQVRYLRPDYAGQSDLTLPHDKSGRNNRYQAKWQHRHIDSTLQAGVDFNQVSDSG					
m958	FDGQVRYLRPDYAGQSDLTLPHDKSGRNNRYQAKWQHRHIDSTLQAGVDFNQVSDSG					
	310	320	330	340	350	360
a958.pep	370	380	390	400	410	420
	YYRDFYGNKEIAGNVNLNRRVWLDYGGRAAGGSILNAGLSVLKYQT LANQSGYKDKPYALM					
m958	YYRDFYGNKEIAGNVNLNRRVWLDYGGRAAGGSILNAGLSVLKYQT LANQSGYKDKPYALM					
	370	380	390	400	410	420
a958.pep	430	440	450	460	470	480
	PRLSADWRKNTGRAQIGVSAQFTRFSHDSRQDGSRLLVVPDIKWD FSNSWGYVRPKLGLH					
m958	PRLSVEWRKNTGRAQIGVSAQFTRFSHDSRQDGSRLLVVPDIKWD FSNSWGYVRPKLGLH					
	430	440	450	460	470	480
a958.pep	490	500	510	520	530	540
	ATYYSLNRFGSQEARRVSRTLPIVNIDSGMTFERNTRMFGGGV LQTL PRLFYNYIPAKS					
m958	ATYYSLNRFGSQEARRVSRTLPIVNIDSGATFERNTRMFGGEV LQTL PRLFYNYIPAKS					
	490	500	510	520	530	540

	490	500	510	520	530	540
a958.pep	550	560	570	580	590	600
m958	QNDLPNFDSSSESSFGYGQLFRENLYYGNDRINTANSLSAAVQSRILDGATGEERFRAGIG 					
a958.pep	610	620	630	640	650	660
m958	QKFYFKNDAVMLDGSGVKKPRSRSDWVAFASSGIGSRFILDSSIHYNQNNDKRAENYAVGA : : :					
a958.pep	670	680	690	700	710	720
m958	SYRPAQGVNLARYKYGRNEKIYLSDGSFYDKLSQLDLSAQWPLTRNLSAVVRYNYGF 					
a958.pep	730	740	750	760	770	780
m958	EAKKPIEVLAGAEYKSSCGCWAGVYAQRYVTGENTYKNAVFFSLQLKDLSSVGRNPADR 					
a958.pep	790	800				
m958	MDVAVPGYIPAHSLSAGRNKPX 					
	790	800				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2935>:

g959.seq

```

1 ATGAAACATCA AACACCTTCT CTTGACCGCC GCCGCAACCG CACTGTTGGG
51 CATTTCGCC CCCGCCTCG CCCCACCGA CGGACACGGC GATGACGACC
101 ACGGACACGC CGCACACCAA CACGGCAAAC AAGACAAAAT CATCAGCCGC
151 GCCAAGCCG AAAAACCGGC TTGGCCGCGT GTCCGGCGCA AAATCACCGA
201 CATCGATCTC GAACACGAGC ACGGCCGTCC GCACATATGAT GTCGAAATCG
251 TCAAAAACGG ACAGGAATAAC AAAGTCGTTG TCGATGCCCG TACCGGCCGC
301 GTGATTTCCCT CCCGCCCGCA CGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2936; ORF 959.ng>:

g959.pep

```

1 MNIKHLLLTA AATALLGISA PALAHHDGHG DDDHGHAHQ HNKQDKIISR
51 AQAEKAAWAR VGGKITDIDL EHDDGRPHYD VEIVKNGQEY KVVDARTGR
101 VISSRRDD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2937>:

m959.seq

```

1 ATGAAACATCA AACACCTTCT CTTGACCTCC GCCGCAACCG CACTGCTGAG
51 CATTTCGCC CCCGCCTCG CCCCACCGA CGGACACGGC GATGACGACC
101 ACGGACACGC CGCACACCAA CACAACAAAC AAGACAAAAT CATCAGCCGC
151 GCCAAGCCG AAAAACCGAGC GTTGGCCGCGT GTCCGGCGCA AAATCACCGA
201 CATCGATCTC GAACACGACA ACGGCCGTCC GCACATATGAT GTCGAAATCG
251 TCAAAAACGG ACAGGAATAAC AAAGTCGTTG TCGATGCCCG TACCGGCCGC
301 GTGATTTCCCT CCCGCCCGCA CGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2938; ORF 959>:

m959.pep

```

1 MNIKHLLLTS AATALLSISA PALAHHDGHG DDDHGHAHQ HNKQDKIISR
51 AQAEKAALAR VGGKITDIDL EHDDGRPHYD VEIVKNGQEY KVVDARTGR
101 VISSRRDD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 959 shows 95.4% identity over a 108 aa overlap with a predicted ORF (ORF 959) from *N. gonorrhoeae*

m959/g959 95.4% identity in 108 aa overlap

	10	20	30	40	50	60
m959.pep	MNIKHL	LTSAA	TALLSISAPALAHHDGHGDDDHGHA	AHQHNQDKI	IISRAQA	KAALAR
g959						
	MNIKHL	LTAAT	ALLGISAPALAHHDGHGDDDHGHA	AHQHGKQDKI	IISRAQA	KAAWAR
	10	20	30	40	50	60
m959.pep	70	80	90	100	109	
g959	VGGKITD	IDLEH	DNGRPHYDVEIVKNGQEYKV	VVVDARTGR	VISSRRDX	
	VGGKITD	IDLEH	DNGRPHYDVEIVKNGQEYKV	VVVDARTGR	VISSRRDX	
	70	80	90	100		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2939>:

a959.seq

```

1 ATGAACCTCA AACGCCCTCT CTTGACCGCC GCCGCAACCG CACTGATGGG
51 CATTTCGCC CCCGCACTCG CCCACCACGA CGGACACCGC GATGACGACC
101 ACGGACACGC CGCACACCAA CACAGCAAAC AGAACAAAAT CATCAGCCG
151 GCCCAAGCCG AAAAAGCAGC GTTGGCGCGT GTCGGCGCA AAATCACCGA
201 CATCGATCTC GAACACGACA ACGGCCGTCC GCACTATGAT GTCGAATCG
251 TCAAAACGG ACAGGAATAC AAAGTCGTTG TCAGATGCCCG TACCGGCCGC
301 GTGATTTCTC CCCGCCCGCA CGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2940; ORF 959.a>:

a959.pep

```

1 MNFKRL
```

~~LLTAAATALMGISA PALAHDGHG DDDHGHAHQ HSKQDKIISR~~

```

51 AQAEKAAALAR VGGKITDIDL EHDNGRPHYD VEIVKNGQEY KV
```

~~VVVDARTGR~~

```

101 VISSRRDX*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 959 shows 94.4% identity over a 108 aa overlap with a predicted ORF (ORF 959) from *N. meningitidis*

a959/m959 94.4% identity in 108 aa overlap

	10	20	30	40	50	60
a959.pep	MNFKRL	LLTAAATALMGISA PALAHDGHG DDDHGHAHQ HSKQDKIISR				
m959						
	MNIKHL	LTSAA	TALLSISAPALAHHDGHGDDDHGHA	AHQHNQDKI	IISRAQA	KAALAR
	10	20	30	40	50	60
a959.pep	70	80	90	100	109	
m959	VGGKITD	IDLEH	DNGRPHYDVEIVKNGQEYKV	VVVDARTGR	VISSRRDX	
	VGGKITD	IDLEH	DNGRPHYDVEIVKNGQEYKV	VVVDARTGR	VISSRRDX	
	70	80	90	100		

g960.seq not found yet

g960.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2941>:

m960.seq

```

1 ATGCAAGTAA ATATTCAGAT TCCCTGTATG CTGTACAGAC GCGGGAGTGT
51 TAAGCCCCCCC TTGTTTGAAAG CTCCGCGGCT CCTGCCGAGC TTACCGAC
101 CCGTTGTGCC CAAGCTCTCT GCTCCCGCGC GCTACATTGT CGACATCCCC
151 AAAAGCAATC TGAAAACCGA AATCGAAAG CTGGCCAAAC AGCCCGAGTA
201 TGCCTATCTG AAACAGCTCC AAGTAGCGAA AAACGTCAAC TGGAACCGAG
251 TGCAACTGGC TTACGATAAA TGGGACTATA AGCAGGAAGG CTTAACCGAG
301 GCGGGTGCAG CGATTATCGC GCTGGCTGTT ACCGTGGTTA CTGCGGGCGC
351 GGGAGTCGGA GCGCACTAG GCTTAAACGG CGCAGCCGCA GCAGCGGCCG
401 ATGCGCGCTT TGCGCTACTC GCTTCTCAGG CTTCCGTATC GCTCATCAAC
451 AATAAAGGCG ATGTCGGCAA AACCTGAAG GAACCTGGCA GAAGCCGCAC
501 GGTAAAAAAT CTGGTTGTAG CGCGCGCAAC GGCAAGCGTA TCCAACAAAC

```

```

551 TCGGTGCCCTC TTCCCTTGCC ACTTGGAGCG AAACCCCTTG GGTAAACAAC
601 CTCAACGTTA ACCTGGCCAA TGCGGGCAGT GCCGCGCTGA TCAACACCGC
651 TGTAAACGGC GGCAGCCTGA AAGACAATCT GGAGGCAAAT ATCCTGGCGG
701 CATTGGTGA TACCGCGCAT GGGGAGGCAG CGAGTAAGAT CAAAGGACTG
751 GATCAGCACT ATGTCGCCCA CAAAATCGCT CATGCCGTAG CGGGCTGTGC
801 GGCTGCAGCG CGCAATAAAGG CCAATGTCA GGACGGCGCG ATCGGTGCGG
851 CTGTGGGTGA GATTGTCGGG GAGCCTTGG TTAAAAAATAC CGATTTAGC
901 GATATGACCC CGGAACAATT AGATCTGGAA GTTAAGAAAA TTACCGCCTA
951 TGCCAAACTT GCGGCAGGTA CAGTTGCAGG CGTAACGGGA GGAGATGTCA
1001 ATACTGCTGC ACAAAACCGCA CAAAACCGGG TAGAAAAATAA TGCGGTTAAA
1051 GCTGTTGTA CTGCTGCAAA AGTGGTTTAT AGGTAGCCA GAAAAGGATT
1101 AAAAACGGG AAAATCAACG TTAGAGATTT AAAACAGACG TTGAAAGACG
1151 AAGGTTATAA TTTAGCCGAC AACCTGACCA CCTTATTGCA CGAAACATTG
1201 GATTGGAACG ATGCCAAAGC CGTTATTGAT ATTGTCGTGCG GAACAGAGCT
1251 GAATCGCGCT AATAAAGGGG AAGCGGCACA AAAGGTCAGA GAAGTTTAG
1301 AAAAACATCG TCCTTATATC CCTATAAAAG GTGCTGTACC GAATATGAGT
1351 ACATACATGA AAAATAATCC TTTTGGAAAAA CAGCTGGCTC AAATTTCAGA
1401 AAAGACAACG CTTCCGACGC AGCAAGGGCA GTCTGTCTTC TTGGTAAAAA
1451 GAAACCAAGG GTTATTAAAA ACCGGTGATA GTTTTATTT AGATGGCCAA
1501 CATAAAAATC ATTTAGAGGT TTTTGATAAA AATGGGAACCT TTAAGTTGT
1551 TCTAAATATG GATGGTTCGG TTAAACCAAAT GAAAACGTGGG GCAGCAAAAG
1601 GTCGTAATT AAACCTAAAA TAG

```

This corresponds to the amino acid sequence <SEQ ID 2942; ORF 960>:

m960.pep

```

1 MQVNIQIPCM LYRRGSVKPP LFEAPRLLPS FTDPVVPKLS APGGYIVDIP
51 KGNLKTEIEK LAKQPEAYL KQLQVAKNVN WNQVQLAYDK WDYKQEGLTR
101 AGAAIIALAV TVVTAGAGVG AALGLNGAAA AAADAFAFL ASQASVSLIN
151 NKGDVGKTLK ELGRSRTVKN LVVAAATAGV SNKLGASSLA TWSETPWVN
201 LNVLNLANAGS AALINTAVNG GSLKDNLLEAN IIAALVNTAH GEAASKIKGL
251 DQHYVAHKIA HAVAGCAAAA ANKGKCQDG AIGAAVGEIVG EALVKNTDFS
301 DMTPEQLDLE VKKITAYAKL AAGTVAGVTG GDVNNTAAQTA QNAVENNAVK
351 AVVITAAKVVY KVARKGLKNG KINVRDLKQT LKDEGYNLAD NLTTLFDETL
401 DWNDAKAVID IVVGTELNRN NKGEAAQKVK EVLEKNRPYI PNKGAVEPNMS
451 TYMKNNPFGK QLAQISEKTT LPTQQGQSVD LVKRNQGLLK TGDRFYLDGQ
501 HKNHLEVFDK NGNFKFVLM DGSLNQMKTG AAKGRKLNLK *

```

a960.seq not found yet

a960.pep not found yet

g961.seq not found yet

g961.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2943>:

m961.seq

```

1 ATGAGCATGA AACACTTTCC AGCCAAAGTA CTGACCACAG CCATCCTTGC
51 CACTTCTGT AGCGGCGCAC TGGCAGCCAC AAGCGACGAC GATGTTAAA
101 AAGCTGCCAC TGTGGCATT GTGCTGCCT ACAACAATGG CCAAGAAATC
151 AACGGTTCA AAGCTGGAGA GACCATCTAC GACATTGGTG AAGACGGCAC
201 AATTACCCCA AAGACGCAA CTGCAGCCGA TGGTGAAGCC GACCGACTTA
251 AAGGTCTGGG TCTGAAAAAA GTCGTGTACTA ACCTGACCAA AACCGTCAAT
301 GAAAACAAAC AAAACGTGCA TGCCAAAGTA AAAGCTGCAG AATCTGAAT
351 AGAAAAGTTA ACAACCAAGT TAGCAGACAC TGATGCCGCT TTAGCAGATA
401 CTGATGCCG TCTGGATGAA ACCACCAACG CCTTGAATAA ATTGGGAGAA
451 AATAAACGA CATTGCTGA AGAGACTAAG ACAAATATCG TAAAAATTGA
501 TGAAAATTA GAAGCCGTGG CTGATACCGT CGACAAGCAT GCGAACAGCAT
551 TCAACGATAT CGCCGATTC TTGGATGAAA CCAACACTAA GCGAGACGAA
601 GCGTCAAA CCGCAATGA AGCCAAACAG ACGGCCGAAG AAACCAAAACA
651 AAACGTCGAT GCCAAAGTAA AAGCTGCAGA AACTGCAGCA GGCAAAGCCG
701 AAGCTGCCG TGGCACAGCT AATACTGCAG CGACAAAGGC CGAAGCTGTC
751 GCTGCAAAAG TTACCGACAT CAAAGCTGAT ATCGCTACGA ACAAAGCTGA
801 TATTGCTAAA AACTCAGCAC GCATCGACAG CTTGGACAAA AACGTAGCTA
851 ATCTGCGAA AGAAACCCGC CAAGGCCCTG CAGAACAAAGC CGCGCTCTCC
901 GGCCTGTTCC AACCTTACAA CGTGGGTCGG TTCATGTAA CGGCTGCACT
951 CGGCGGCTAC AAATCCGAAT CGGCAGTCGC CATCGGTACC GGCTTCCGCT
1001 TTACCGAAAAA CTTTGGCCGC AAAGCAGGCG TGGCAGTCGG CACTTCGTC
1051 GGTTCTTCCG CAGCCTACCA TGTCGGCGTC AATTACGGAGT GGTAA

```

This corresponds to the amino acid sequence <SEQ ID 940; ORF 2944>:

m961.pep

```

1 MSMKHFPACK LTTAILATFC SGALAATSD DVKKAATVAI VAAYNNNGOEI

```

51 NGFKAGETIY DIGEDGTITO KDATAADVEA DDFKGLGLKK VVTNLTKTVN
 101 ENKQNVDAKV KAAESEIEKL TTKLADTDAA LADTDAALDE TTNALNKLG
 151 NITTFAEETK TNIVKIDEKL EAVADTVDKH AEAFTNDIADS LDETNTKADE
 201 AVKTANEAKQ TAEETKQNVD AKVKAETAA GKAEEAAAGTA NTAADKAEAV
 251 AAKVTDIKAD IATNKADI AKSARIDSLDK NVANLRKETR QGLAEQAALS
 301 GLFOPYNVGR FNVTAAVGGY KSESAVAIGT GFRFTENFAA KAGVAVGTSS
 351 GSSAAYHVGV NYEW*

a961.seq not found yet
 a961.pep not found yet

9972.seq not found yet
 9972.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2945>:
~~m972.seq~~

1 TTGACTAACAA GGGGGGGAGC GAAATTAAAA ACCAATTCCA AGAGTAGTGA
 51 ACGAATGAGT GAAGTTGAAT ATTTCTCACCA CTTTATATCG GACGGAAAAG
 101 GGAAGCTTTT AGAAATTCCG CAGCGAAGAG GTAAGCAAGA CGGGGTTTTT
 151 GTTGATTGGA TTTCATTCA C ATTCCATGAA GATACTTTAC TGAAAGTTTC
 201 CGGTTGCCCT TTATTTCTG ATGCTGAATA CATGTATGTA TTAAGCAGAA
 251 AGCTGGAAGA AATTCTAGGT TTTGGCATAA CGCGCAAATG CAAATCAAGG
 301 GGCAACAAAT TCTATGAATC CATGTATAGG TTAGGTTCGG ATGATGTTGA
 351 TTATGGAGAG GTGCATTTCG GARGTCAAGCG CAATACTGTT TTAGTTGAGT
 401 TGAAAGGTAC TGGTGCAGC GTTGCAGTC CGGGTTGGGA GTTGAGGCTA
 451 AAGCAGTTTC TCGATGATTC GATAAGGACA AGAATAACGC GAATTGACCT
 501 AGCACTTGAT TTTTTGATG GAGAGTACAC GCCGGATCAG GCGTTGTTAG
 551 ATCACGATAA TGGTTTTTTT GATAACAGCA ATCAAAGGCC GAAATCTGAA
 601 ACGATCGGTA CGGCTTGGCG GAATGAGGAC GGGAGCGGCA AGACATTAA
 651 TGTAGGTCGC AAGAAAAATT CTCGTTTGT TCGTGTGTTAT GAGAAAGGCA
 701 GGCAGCTTGG AGATAAAAGAA AGCAAATGGG TAAGGTTCGA GATCCAGTTT
 751 ATTATGGAG ATATAGAAAT ACCCTGGAT ATTTTAATAA ATCAGGGTT
 801 GTATTTCTGT GGAGCTTTTC CAATTTGAG AAAATTAAA AATATGCCGG
 851 TTCCCGAAAG GTTGTACAG AGAAAAGAAA AGCTTAATT AACTTTCGAG
 901 CATAAAATTGC ATTACCGGAA AAACCGGGTT GGAAAACTGG TCAATTTCAT
 951 GATTGAAATG GTTTTGATA ATAGCGAAAT TGTGGAATCT TAAAGGCAG
 1001 ATTCGGGATT TCCCCAAGGA TTAGAACCTG AAAAATATGC TCTGGAAATG
 1051 TTAAGGGACG GTTGTAAACA CGGTTTTATT CATGAACAGC CGGATATTGA
 1101 TTGGAATTA GAACTTGATG AATTGGGGGT TATTGTTTT AAAAATTCTG
 1151 ACAAAATTCGA TAGGGAAAAA AGGCTTTTA GTCTGTGATTA TGATGTCGAG
 1201 AAAGAAAGGA AATATCAGGA ATATTTAAGT AAAGTTTATC ATCAAATGT
 1251 AGATTATGAT TATTTTAA

This corresponds to the amino acid sequence <SEQ ID 2946; ORF 972>:
~~m972.pep~~

1 LTNRGGAALK TXSKSSERMS EVEYFSHFIS DGKGKLLIEIP QRGGKQDGVF
 51 VDWISFTFHE DTLLKVSGCP LFSDAEYMYV LSRKLEELIG FGITRKCKSR
 101 GNKFYFESMYR LGSDDVDYGE VHFGXQRNTV LVELKGTGCS VASPGWELRL
 151 KQFLDDDSIRT RITRIDLALD FFDGEYTPDQ ALLDHDNGFF DNSNQRPKSE
 201 TIGTAWRNED GSGKTFYVGR KKNSRFVRVY EKGRQLGDKE SKWVRFEIQF
 251 NYGDIEIPLD ILINQGSYFC GAFFPICRKFK NMPVPERFDQ RKKKLNLTFE
 301 HKLHYAKNAV GKLVNFMIEM GFDNSEIVES LKADSGFPKG LEPEKYALEM
 351 LRDGLKHGFI HEQPDIDLEI ELDELGVIAF KNSDKFDREK RLFSPDYDVE
 401 KERKYQEYLS KVYHQNVYD YF*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2947>:
~~a972.seq~~

1 TTGACTAACAA GGGGGGGAGC GAAATTAAAA ACCAATTCCA AGAGTAGTGA
 51 ACGAATGAGT GAAGTTGAAT ATTTCTCACCA CTTTATATCG GACGGAAAAG
 101 GGAAGCTTTT AGAAATTCCG CAGCGAAGAG GTAAGCAAGA CGGGGTTTTT
 151 GTTGATTGGA TTTCATTCA C ATTCCATGAA GATACTTTAC TGAAAGTTTC
 201 CGGTTGCCCT TTATTTCTG ATGCTGAATA CATGTATGTA TTAAGCAGAA

251 AGCTGGAAGA AATTCTAGGT TTGGCATAA CGCGCAAATG CAAATCAAGG
 301 GGCAACAAAT TCTATGAATC CATGTATAGG TTAGGTTTCGG ATGATGTTGA
 351 TTATGGAGAG GTGCATTTCG GAGGTCAAGCG CAATACTGTT TTAGTTGAGT
 401 TGAAAGGTAC TGGTTGCAGC GTTGCAAGTC CGGGTTGGGA GTTGAGGCTA
 451 AAGCAGTTTC TCGATGATTC GATAAGGACA AGAATAACGC GAATTGACCT
 501 AGCACTTGAT TTTTTGATG GAGAGTACAC GCCGGATCAG GCCTTGTAG
 551 ATCACGATAA TGTTTTTTT GATAACAGCA ATCAAAGGCC GAAATCTGAA
 601 ACGATCGGTA CGGCTTGGCG GAATGAGGAC GGGAGCGGCA AGACATTTA
 651 TGTAGGTGCG AAGAAAAATT CTCGTTTGT TCGTGTAT GAGAAAGGCA
 701 GGCAGCTTGG AGATAAAGAA AGCAAATGGG TAAGGTTCGA GATCCAGTTT
 751 ATTATGGAG ATATAGAAAT ACCCTTGGAT ATTTTAATAA ATCAGGGTTC
 801 GTATTTCTGT GGAGCTTTC CAATTTGAG AAAATTAAA AATATGCCGG
 851 TTCCCGAAAG GTTGATCAG AGAAAGAAAA CGCTTAATT AACTTCGAG
 901 CATAAAATTGC ATTACCGCAA AACACGGTT GGAAAGACTGG TCAATTTCAT
 951 GATTGAAATG GGTTTGATA ATAGCGAAAT TGTGGAATCT TAAAGGCAG
 1001 ATTCCGGGATT TCCCCAAAGGA TTAGAACCTG AAAAATATGC TCTGGAAATG
 1051 TTAAGGGACG GTTGAAACAC CGGTTTTATT CATGAACAGC CGGATATTGA
 1101 TTGGAAATT GAACTTGATG AATTGGGGGT TATTGCTTT AAAAATTCTG
 1151 ACAAAATTGCA TAGGGAAAAA AGGCTTTTA GTCTGATTA TGATGTCGAG
 1201 AAAGAAAGGA AATATCAGGA ATATTTAAGT AAAGTTTATC ATCAAAATGT
 1251 AGATTATGAT TATTTTAA

This corresponds to the amino acid sequence <SEQ ID 2948; ORF 972.a>:

a972.pep

```

1 LTNRGGAALK TNSKSSERMS EVEYFSHFIS DGKGKLLEIP QRKGQDGVF
51 VDWISFTFHE DTLLKVSGCP LFSDAEYMYV LSRKLEELIG FGITRKCKSR
101 GNKFYESMYR LGSDDDVDYGE VHFGGQRNTV LVELKGTCGS VASPGWELRL
151 KQFLDDDSIRT RITRIDALD FFDGEYTPDQ ALLDHDNGFF DNSNQRPKSE
201 TIGTAWRNED GSGKTFYVGR KKNSRFVRVY EKGRQLGDKE SKWVRFIEIQF
251 NYGDIIEIPLD ILINQGSYFC GAFFICRKFK NMPPVERFDQ RKKTLNLTFE
301 HKLHYAKNAV GKLVNFMIEG GFDNSEIVES LKADSGFPKG LEPEKYALEM
351 LRDGLKHGFI HEQPDIDLEI ELDELGVIAF KNSDKFDREK RLFSPDYDVE
401 KERKYQEYLS KVYHQNVYD YF*

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m972/a972 99.3% identity in 422 aa overlap

	10	20	30	40	50	60	
m972.pep	LTNRGGAKLTXSKSSERMSEVEYFSHFISDGKGKLLEIPQRKGQDGVFVWDWISFTFHE						
a972	LTNRGGAKLTKNSKSSERMSEVEYFSHFISDGKGKLLEIPQRKGQDGVFVWDWISFTFHE	10	20	30	40	50	60
m972.pep	DTLLKVSGCPLFSDAEYMYVLSRKLEEILGFGITRKCKSRGNKFYESMYRLGSDDVDYGE	70	80	90	100	110	120
a972	DTLLKVSGCPLFSDAEYMYVLSRKLEEILGFGITRKCKSRGNKFYESMYRLGSDDVDYGE	70	80	90	100	110	120
m972.pep	VHFGXQRNTVLVELKGTGCSVASPGWELRLKQFLDDDSIRTRITRIDLALDFDGEYTPDQ	130	140	150	160	170	180
a972	VHFGGQRNTVLVELKGTGCSVASPGWELRLKQFLDDDSIRTRITRIDLALDFDGEYTPDQ	130	140	150	160	170	180
m972.pep	ALLDHNGFFDNSNQRPKSETIGTAWRNEDGSGKTFYVGRKKNSRFVRVYEKGRQLGDKE	190	200	210	220	230	240
a972	ALLDHNGFFDNSNQRPKSETIGTAWRNEDGSGKTFYVGRKKNSRFVRVYEKGRQLGDKE	190	200	210	220	230	240
m972.pep	SKWVRFIEIQFNYGDIIEIPLDILINQGSYFCGAFFICRKFKNMPVPERFDQRKKLNLTFE	250	260	270	280	290	300
a972	SKWVRFIEIQFNYGDIIEIPLDILINQGSYFCGAFFICRKFKNMPVPERFDQRKKLNLTFE	250	260	270	280	290	300

	310	320	330	340	350	360
m972.pep	HKLHYAKNAVKGKLVNFMIEMGFDNSEIVESLKADSGFPKGLPEKYALEMLRDGLKHGFI					
a972						
	310	320	330	340	350	360
m972.pep	HEQPDIDLEIELDELGVIAFKNSDKFDREKRLFSPDYDVEKERKYQEYLSKVYHQNVYD					
a972						
	370	380	390	400	410	420
m972.pep	HEQPDIDLEIELDELGVIAFKNSDKFDREKRLFSPDYDVEKERKYQEYLSKVYHQNVYD					
a972	370 380 390 400 410 420					
m972.pep	YFX					
a972						
	YFX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2949>:
 g973.seq

```

 1 ATGGACGGCG CACAACCGAA AACAAATT TTGAAACGCC TGATTGCCG
 51 actCGCCCGC GAACCCGATT CCGCCGAAGA CGTATTAAC CTGCTTCGGC
 101 AGGCGCACGA ACAGGAAGTT TTTGATGCCG ACACACTGAC CCGGCTGGAA
 151 AAAGTATTGG ACTTTGCCGA GCTGGAAGTG CGCGATGCAG TGATTACCG
 201 CAGCCGCATG AACGTATTGA AAGAAAACGA CAGCATCGAA CGCATCACCG
 251 CCTACGTAT CGATAACCGCC CATTGCGCT TCCCCGTAT CGCGAAGAC
 301 AAAGACGAAG TTTGGGCAT TTTGCACGCC AAAGACCTGC TCAAATATAT
 351 GTTCAACCCC GAGCAGTTCC ACCTGAAATC CGTCTGCGC CCTGCCGTTT
 401 TCGTGCCGA AGGCAAATCT TTGACCGCCC TTTAAAAGA GTTCCGCGAA
 451 CAGCGCAACC ATATGGCAAT CGTCATCGAC GAATACGGCG GCACGTCGGG
 501 TTTGGTCACC TTTGAAGACA TCATCGAGCA aatcgctggc gacaTCGAAG
 551 ACGAGTTTGA CGAACGACGAA AGCGccgacg acatCCACTC cgTTTccgCC
 601 GAACGCTGGC GCATCCacgc ggctaACCGAA ATCGAAAGaca TCAACGCCCTT
 651 TTTCCGGTAGC GAatacggca gcgaagaagc cgacaccatc ggccggctTGG
 701 TCATTCAGGA ATTGGGACAC CTGCCGTGC GCGGGAAAA AGTCCTTAtc
 751 ggcgGTTTGC agttcacgt CGCCCGCGCC GACAACCGCC GCCTGCACAC
 801 GCTGATGGCG ACCCGCGTGA AGTAAGCAGA GCCTGCCGc accggcgtt
 851 CTGCaCAGTT TAG
  
```

This corresponds to the amino acid sequence <SEQ ID 2950; ORF 973.ng>:
 g973.pep

```

 1 MDGAQPKTNF FERLIARLAR EPDSAEDVLN LLRQAHEQEV FDADTLTRLE
 51 KVLDFAELEV RDAMITRSRM NVLKENDSIE RITAYVIDTA HSRFPVIGED
 101 KDEVLGILHA KDLLKYMNP EQFHLKSVLR PAVFVPEGKS LTALLKEFRE
 151 QRNHMAIVID EYGGTSLVLT FEDIIEQIVG DIEDEFDEDE SADDIHSVSA
 201 ERWRIHAATE IEDINAFFGT EYGSEEADTI GGLVIQELGH LPVRGEKVLI
 251 GGLQFTVARA DNRRILHTLMA TRVK*
  
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2951>:
 m973.seq

```

 1 ATGGACGGCG CACAACCGAA AACGAATT TTGAAACGCC TGATTGCCG
 51 ACTCGCCCGC GAACCCGATT CCGCCGAAGA CGTATTAAC CTGCTTCGGC
 101 AGGCGCACGA GCAGGAAGTT TTTGATGCCG ATACGCTTT AAGATTGGAA
 151 AAAGTCTCG ATTTTCCGA TTTGGAAGTG CGCGACGCAG TGATTACCG
 201 CAGCCGTATG AACGTTTAA AAGAAAACGA CAGCATCGAG CGCATCACCG
 251 CCTACGTAT CGATAACCGCC CATTGCGCT TCCCCGTAT CGCGAAGAC
 301 AAAGACGAAG TTTGGGCAT TTTGCACGCC AAAGACCTGC TCAAATATAT
 351 GTTTAACCCC GAGCAGTTCC ACCTCAAATC CATTCTCCGC CCCGCCGTCT
 401 TCGTCCCCGA AGGCAAATCG CTGACCGCCC TTTAAAAGA GTTCCGCGAA
 451 CAGCGCAACC ATATGGCGAT TGTATCGAC GAATACGGCG GCACATCCGG
 501 CTTGGTCACC TTTGAAGACA TCATCGAGCA AATCGTCGGC GAAATCGAAG
 551 ACGAGTTTGA CGAACGACGAT AGCGCCGACA ATATCCATGC CGTTTCTTCm
 601 GaACGcTGCG GCATCCATGC AGCTACCGAA ATCGAAGACA TCAACACCTT
  
```

651 CTTCGGCACG GAATACAGCA ~~k~~CGAAGAACG CGACACCATT GGGGCCCTGG
701 TCATTCAGA GTTGGGACAT CTGCCCCGTGC GCGGCGAAAA AGTCCTTATC
751 GGC GGTTTG AGTTCACCGT CGCACGCGCC GACAACCGCC GCCTGCATAAC
801 GCTGATGGCG ACCCGCGTGA AGTAA

This corresponds to the amino acid sequence <SEQ ID 2952; ORF 973>:

m973.pep

1	MDGAQPKTNF	FERLIARLAR	EPDSAEDVNL	LLRQAHEQEV	FDADTLLRLE
51	KVLDFSDLEV	RDAMITRSRM	NVLKENDSIE	RITAYVIDTA	HSRFPVIGED
101	KDEVLGILHA	KDLLKYMFPNP	EQFHLKSILR	PAVFVPEGKS	LTALLKEFRE
151	QRNHMAIVID	EYGGTSQLVT	FEDIIEQIVG	EIEDEFDEDD	SADNIHAVSS
201	ERWRRIHAATE	IEDINTFFGT	EYSXEEADTI	GGLVIQELGH	LPVRGEKVLI
251	GGLOFTVARA	DNRRLLHTLMA	TRVK*		

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 973 shows 95.6% identity over a 274 aa overlap with a predicted ORF (ORF 973.ng) from *N. gonorrhoeae*:

m973/g973

	10	20	30	40	50	60
m973 . pep	MDGAQPKTNFFERLIARLAREPDSAEDVLNLLRQAHEQEVFDADTLRLEKVLDFSDLEV					
g973	MDGAQPKTNFFERLIARLAREPDSAEDVLNLLRQAHEQEVFDADTLRLEKVLDFAELEV					
	10	20	30	40	50	60
m973 . pep	RDAMITRSRMNVLKENDSIERITAYVIDTAHSRFPVIGEDKDEVLGILHAKDLLKYMFP					
g973	RDAMITRSRMNVLKENDSIERITAYVIDTAHSRFPVIGEDKDEVLGILHAKDLLKYMFP					
	70	80	90	100	110	120
m973 . pep	EQFHLKSIILRPAVFVPEGKSLTALLKEFREQRNHMAIVIDEYGGTSGLVTFEDIIEQIVG					
g973	EQFHLKSVLRPAVFVPEGKSLTALLKEFREQRNHMAIVIDEYGGTSGLVTFEDIIEQIVG					
	130	140	150	160	170	180
m973 . pep	EIEDEFDEDSDADNIHAVSSERWRIGHAATEIEDINTFFGTEYSXEEADTIGGLVIQELGH					
g973	DIEDEFDEDESADDIHSVSAERWRIGHAATEIEDINAFFGTEYGSSEEADTIGGLVIQELGH					
	190	200	210	220	230	240
m973 . pep	LPVRGEKVLIGGLQFTVARADNRRLHTLMATRVKK					
g973	LPVRGEKVLIGGLQFTVARADNRRLHTLMATRVKK					
	250	260	270			
m973 . pep	LPVRGEKVLIGGLQFTVARADNRRLHTLMATRVKK					
g973	LPVRGEKVLIGGLQFTVARADNRRLHTLMATRVKK					
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 2953>:

a973.seq

1	ATGGACGGCG	CACAACCGAA	AACAAATTTC	TTTGAACGCC	TGATTGCCGC
51	ACTCGCCCGC	GAACCCGATT	CCGCCGAAGA	CGTATTGACC	CTGTTGCGCC
101	AAGCGCACGA	ACAGGAAGTA	TTTGATGCGG	ATACGCTTT	AAGATTGGAA
151	AAAGTCCTCG	ATTTTTCTGA	TTTGGAAAGTG	CGCGACGCGA	TGATTACGCG
201	CAGCCGTATG	AACGTTTAA	AAGAAAACGA	CAGCATCGAA	CGCATCACCAG
251	CCTACGTTAT	CGATAACGCC	CATTGCGCT	TCCCCGTCAT	CGGTGAAGAC
301	AAAAGACGAAG	TTTGGGTAT	TTTGACGCC	AAAGACCTGC	TCAAATATAT
351	GTTCACCCCC	GAGCAGTTCC	ACCTCAAATC	GATATTGCGC	CCTGGCGTCT
401	TCGTCCCCGA	AGGCAAAATCG	CTGACCGGCC	TTTTAAAAAGA	GTTCCCGGAA
451	CAGCGCAACC	ATATGGCAAT	CGTCATCGAC	GAATACGGCG	GCACCGTCGGG
501	TTTGGTAACT	TTTGAAGACA	TCATCGAGCA	AATCGTCGGC	GACATCGAAG
551	ATGAGTTTGA	CGAAGACGAA	AGCGCGGACA	ACATCCACGC	CGTTTCCCGCC

601 GAA CGCTGGC GCATCCACGC GGCTACCGAA ATCGAAGACA TCAACGCCTT
 651 TTT CGGCACG GAATACAGCA GCGAAGAACG CGACACCATC GCGGGCCTGG
 701 TCATT CAGGA ATT GGGACAC CTGCCC GTGC GCGGCGAAAA AGTCCTTATC
 751 GGC GGTTTG AGTT CACCGT CGCCCGCGCC GACAACCGCC GCCTGCATAC
 801 GCTGATGGCG ACCCGCGTGA AGTAA

This corresponds to the amino acid sequence <SEQ ID 2954; ORF 973.a>:

a973.pep

1 MDGAQPKTNF FERLIARLAR EPDSAEDVLT LLRQAHEQEV FDADTLLRLE
 51 KVLDLFSDELV RDAMITRSRM NVLKENDSIE RITAYVIDTA HSRFPVIGED
 101 KDEVLGILHA KDLKYMFMNP EQFHLKSILR PAVFVPEGKS LTALLKEFRE
 151 QRNHMAIVID EYGGTSGLVT FEDIIEQIVG DIEDEDEFDEDE SADNIHAVSA
 201 ERWRIHAATE IEDINAFFGT EYSSEEADTI GGLVIQELGH LPVRGEKVLI
 251 GGLQFTVARA DNRLHTLMA TRVK*

m973/a973 97.8% identity in 274 aa overlap

	10	20	30	40	50	60
m973.pep	MDGAQPKTNFFERLIARLAREPDSAEDVLTLLRQAHEQEVFDADTLLRLEKVLDLFSDELV					
a973	MDGAQPKTNFFERLIARLAREPDSAEDVLTLLRQAHEQEVFDADTLLRLEKVLDLFSDELV	10	20	30	40	50
		10	20	30	40	50
		70	80	90	100	110
m973.pep	RDAMITRSRMNVLKENDSIERITAYVIDTAHSRFPVIGEDKDEVLGILHAKDLLKYMFMNP					120
a973	RDAMITRSRMNVLKENDSIERITAYVIDTAHSRFPVIGEDKDEVLGILHAKDLLKYMFMNP	70	80	90	100	110
		70	80	90	100	110
		130	140	150	160	170
m973.pep	EQFHLKSILRPAPVFPEGKSLTALLKEFREQRNHMAIVIDEYGGTSGLVTFEDIIEQIVG					180
a973	EQFHLKSILRPAPVFPEGKSLTALLKEFREQRNHMAIVIDEYGGTSGLVTFEDIIEQIVG	130	140	150	160	170
		130	140	150	160	180
		190	200	210	220	230
m973.pep	EIEDEFDEDDSADNIHAVSSERWRIHAATEIEDINTFFGTEYSXEEADTIGGLVIQELGH					240
a973	DIEDEFDEDESADNIHAVSAERWRIHAATEIEDINAFFGT EYSSEEADTIGGLVIQELGH	190	200	210	220	230
		190	200	210	220	240
		250	260	270		
m973.pep	LPVRGEKV LIGGLQFTVARADNRRLHTLMATRVKX					
a973	LPVRGEKV LIGGLQFTVARADNRRLHTLMATRVKX	250	260	270		
		250	260	270		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2955>:

g981.seq

1 ATGAAAAAAAT GGATTGCCGC CGCCCTTGCC TGTTCCGCAC TCGCGCTGTC
 51 TGCCTGGCG GGTCAAGGCA AAGATGCCGC CGCCCTGCC GCCAACCCCG
 101 GCAAAGTGT A CCGCGTGGCT TCCAACGCCG AGTTTGCCCC CTTTGAATCT
 151 TTAGACTCGA AAGGCAATGT CGAAGGTTTC GACGTGGATT TGATGAACGC
 201 GATGGCGAAG GCGGGCAATT TAAAATCGA ATTCAAACAC CAGCCGTGGG
 251 ACAGCCTTTT CCCCCCTGGA AACAAACGGCG ATGCGGACGTT TGTGATGTCG
 301 GGGCTAACCA TTACCGACGA CGCCTAACAG TCTATGGATT TCAGCGACCC
 351 GTATTTGAA ATCACCAAG TCGTCTCGT TCCGAAAGGC AAAAAAGTAT
 401 CTTCTCCGA AGATTGAAA AAGATGAACA AAGTCGGCGT GGTTACCGGC
 451 CACACGGCG ATTTCTCCGT TTCCAAACTC TTGGGCAACG ACAATCCGAA
 501 AATCGCGCGC TTCAAAACG TCCCCCTGAT TATCAAAGAA CTGGAAAACG
 551 GCGGCTTGGGA TTCCGTGGTC AGCGACAGCG CGGTACATCGC CAATTATGTG
 601 AAAAACAAACC CGGCCAAAGG AATGGACTTC GTTACCCCTGC CCGACTTCAC
 651 CACCGAACAC TACGCCATCG CGGTACGCAA AGGCGACGAA GCAACCGTCA
 701 AAATGCTGAA CGATGCGTTG GAAAAAGTAC GCGAAAGCGG CGAATACGAC
 751 AAGATCTACG CCAAATATTT TGCCAAAGAG GGC GGACAGG CTGCGAAATA
 801 A

This corresponds to the amino acid sequence <SEQ ID 2956; ORF 981.ng>:

g981.pep

```

1 MKKWIAAAALA CSALALSACG GQGKDAAPPA ANPGKVYRVA SNAEFAPPES
51 LDSKGNVEGF DVDLMNAMAK AGNFKIEFKH QPWDLSLFPAL NNGDADVVMS
101 GVTITDDRQK SMDFSDPYFE ITQVVLVPKG KKVSSEDLK KMNKVGVVTC
151 HTGDFSVSKL LGNDNPKIAR FENVPLIIKE LENGGLDSVV SDSAVIANYV
201 KNNPAKGMDF VTLPDFTEH YGIAVRKGD EATVKMLNDAL EKVRESGEYD
251 KIYAKYFAKE GGQAAK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2957>:

m981.seq

```

1 ATGAAAAAAAT GGATTGCCGC CGCCCTGCC TGTTCCGCC TCGCGCTGTC
51 TGCCTGCCGC GGTCAAGGGCA AAAGATAACCGC CGCGCCTGCC GCCAACCCCG
101 ACAAAAGTGA CCGCGTGGCT TCCAACGCCG AGTTTGCCCC CTTTGAATCT
151 TTAGACTCGA AAGGCAATGT CGAAGGTTTC GATGTGGATT TGATGAAACGC
201 GATGGCGAAG GCGGGCAATT TAAAAATCGA ATTCAAACAC CAGCCGTGGG
251 ACAGCCCTTT CCCCGCCTTA AACAAACGCCG ATGCGGACGT TGTGATGTCG
301 GGCCTAACCA TTACCGACGA CCGCAAACAG TCTATGGACT TCAGCGACCC
351 GTATTTGAA ATCACCCAAG TCGTCCTCGT TCCGAAAGGC AAAAAAGTAT
401 CTTCTTCCGA AGATTGAAA AACATGAACA AAGTCGGCGT GGTAACCGGC
451 TACACGGCGC ATTCCTCCGT ATCCAAACTC TTGGGCAACG ACAATCCGAA
501 ATACGGCGGC TTTGAAAACG TTCCCCTGAT TATCAAAGAA CTGGAAAACG
551 GCGGCTTGGGA TTCCGTGGTC AGCGACAGCG CGGTCAATGCC CAATTATGTG
601 AAAACAAATC CGGCCAAAGG GATGGACTTC GTTACCTGCG CCGACTTCAC
651 CACCGAACAC TACGGCATCG CGGTACGCAA AGGGCACGAA GCAACCGTCA
701 AAATGCTGAA CGATGCGTTG GAAAAAGTAC GCGAAAGCGG CGAATACGAC
751 AAGATTTACG CCAAATATTT TGCAAAAGAA GACGGACAGG CCGCAAAATA
801 A

```

This corresponds to the amino acid sequence <SEQ ID 2958; ORF 981>:

m981.pep

```

1 MKKWIAAAALA CSALALSACG GQGKDTAAPA ANPDKVYRVA SNAEFAPPES
51 LDSKGNVEGF DVDLMNAMAK AGNFKIEFKH QPWDLSLFPAL NNGDADVVMS
101 GVTITDDRQK SMDFSDPYFE ITQVVLVPKG KKVSSEDLK KMNKVGVVTC
151 YTGDFSVSKL LGNDNPKIAR FENVPLIIKE LENGGLDSVV SDSAVIANYV
201 KNNPAKGMDF VTLPDFTEH YGIAVRKGD EATVKMLNDAL EKVRESGEYD
251 KIYAKYFAKE DGQAAK*

```

m981/g981 98.1% identity in 266 aa overlap

981.pep	10 20 30 40 50 60
	MKKWIAAAALCSALALSACGGQGKDTAAPAANPDKVYRVASNAEFAPFESLDSKGNVEF : : : : : : : : : :
9981	10 20 30 40 50 60
	MKKWIAAAALCSALALSACGGQGKAAAAPAAANPGKVYRVASNAEFAPFESLDSKGNVEF : : : : : : : : : :
981.pep	70 80 90 100 110 120
	DVDLMNAMAKAGNFKIEFKHQPWDLSLFPALNNNGDADVVMSGVTITDDRQSMDFSDPYFE : : : : : : : : : :
9981	70 80 90 100 110 120
	DVDLMNAMAKAGNFKIEFKHQPWDLSLFPALNNNGDADVVMSGVTITDDRQSMDFSDPYFE : : : : : : : : : :
981.pep	130 140 150 160 170 180
	ITQVVLVPKGKKVSSSEDLKNMNKVGVTGTYGDFSVSKLLGNDNPKIARFENVPLIIKE : : : : : : : : : :
9981	130 140 150 160 170 180
	ITQVVLVPKGKKVSSSEDLKKMNKVGVTGHTGDFSVSKLLGNDNPKIARFENVPLIIKE : : : : : : : : : :
981.pep	190 200 210 220 230 240
	LENGGLDSVSDSAVIANYVKNNPAKGMDFVTLPDFTEHYGIAVRKGD EATVKMLNDAL : : : : : : : : : :
9981	190 200 210 220 230 240
	LENGGLDSVSDSAVIANYVKNNPAKGMDFVTLPDFTEHYGIAVRKGD EATVKMLNDAL : : : : : : : : : :
981.pep	250 260
	EKVRESGEYDKIYAKYFAKEDGQAAXX : : : : : : : : :
9981	250 260
	EKVRESGEYDKIYAKYFAKEGGQAAXX : : : : : : : : :

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2959>:

a981.seq

```

1 ATGAAAAAAAT GGATTGCCGC CGCCCTTGGC TGTTCCCGCGC TCGCGCTGTC
51 TGCCTGCCGC GGTCAAGGTA AAGATGCCGC CGCGCCCGCC GCAAATCCCG
101 ACAAAAGTGT CCGCGTGGCT TCCAACGCCG AGTTTGCCCC CTTTGAATCT
151 TTAGACTCGA AAGGCAATGT CGAAGGTTTC GATGTTGGATT TGATGAACGC
201 GATGGCGAAG GCGGGCAATT TTAAAATCGA ATTCAAACAC CAGCCGTGGG
251 ACAGCCTTT CCCCGCCTTG AACAAACGGCG ATGCGGACGT TGTGATGTCC
301 GCGCTAACCA TTACCGACGA CCGCAAAACAG TCTATGGACT TCAGCGACCC
351 GTATTTGAA ATCACCCAAAG TCGTCCTCGT TCCGAAAGGC AAAAAAAATAT
401 CTTCTTCGA AGATTTGAAA AACATGAACA AAGTCGGCGT GGTAAACCGGC
451 TACACGGCG ATTCTTCCCGT ATCCAAACTC TTGGGCAACG ACAACCCGAA
501 AATCGCGCG TTTGAAAACG TTTCTCTGAT TATCAAAGAA CTGGAAAACG
551 GCGGCTTGGA TTCCGTGGTC AGCGACAGCG CAGTCATCGC CAATTATGTG
601 AAAAACAAATC CGACCAAAGG GATGGACTTC GTTACCCCTGC CCGACTTCAC
651 CACCGAACAC TACGGCATCG CGGTACGCAA AGGCAGCAGA GCAACCGTCA
701 AAATGCTGAA CGATGCGTTG AAAAAAGTAC GCGAAAGCGG CGAATACGAC
751 AAAATCTACG CCAAATATTT TGCAAAAGAA GACGGACAGG CCGCAAAATA
801 A

```

This corresponds to the amino acid sequence <SEQ ID 2960; ORF 981.a>:

a981.pep

```

1 MKKWIAAAALA CSALALSACG GQGKDAAPPA ANPDVKYRVA SNAEFAPFES
51 LDSKGNVEGF DVDLMNAMAK AGNFKIEFKH QPWDLSFPAL NNGDADVVM
101 GVTITDDRQK SMDFSDPYFE ITQVVLVPKG KKISSSEDLK NMNKVGVV
151 YTGDFSVSKL LGNDNPKIAR FENVPLIIKE LENGGLDSVV SDSAVIANYV
201 KNNPTKGMDF VTLPDFTEHY GIAVRKGDE ATVKMLNDAL KKVRESGEYD
251 KIYAKYFAKE DGQAAK*

```

m981/a981 98.5% identity in 266 aa overlap

	10	20	30	40	50	60
m981.pep	MKKWIAAAALAC	SALALSACG	GQGKDTAAPA	ANPDVKYRVA	SNAEFAPFES	LD SKGNVEGF
a981						
m981.pep	DV DLMNAMAKA	GAGNFKIEFKH	QPWDLSFPAL	NNGDADVVM	SGVTITDDRQK	SMDFSDPYFE
a981						
m981.pep	ITQVVLVPKGKK	VSSSEDLKNM	NKVGVV	TGYTGDFSV	SKLLGNDNP	KIARFENVPLIIKE
a981						
m981.pep	LENGGLDSVV	SDSAVIANYV	KNNPAKGMD	FVTLPDFTT	EHYGIAVRK	DEATVKMLNDAL
a981						
m981.pep	EKVRESGEYDKI	YAKYFAKE	DGQAAKX			
a981						
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2961>:

g982.seq

```

1 atcgcacatcgcaaaaccttcgattcgacaatcgattccctccaaaaatggt
51 caacggcgTg aatattttgc cggccgcCga ttgggttagcC ttggGGcgcCA
101 AAGGCCGCAA CGTGGTGGTT GACCGCGCTT TCGGCCGCCGCACATCACC
151 AAAGACGGCG TAACCGTCGC CAAAGAAATC GAACTGAAAG ACAAGTTGA
201 AAATATGGGC GCGCAAATGG TAAAAGAAGT CGCGTCCAAA ACCAACgaCg
251 tagCCGgcga cggtagact accgCCACCG TATTGGCACA ATCCATCGTT
301 GCCGAAggcA TGAAATACGT TACCGCCGGC ATGAGACCCGA CGCATCTGAA
351 ACAGCGGCATC GACAAAGccg ttgcggCTtt ggttgAAAGAg ctGAAAAAAC
401 TCGCCAACC TTGCGATACT TCCAAAGAAA TCGCCCAAGT CGGCTCGATT
451 TCCGCCAACT CCGACGAACA AGtcgGCGCG ATTATCGCCG AAGCGATGGA
501 AAAAGTCGGC AAAGAAAGgcg tgattacCGT TGAAGACGGC AAATCTTG
551 AAAACGAGCT GGACGTGGTT GAAGGTATGC AGTTCGACCG CGGCTACCTG
601 TCCCCTTACT TTATCAACGA CGCGGAAAAAA CAAATCGCCG GTCTGGACAA
651 TCCGTTTGGT TTGCTGTTCG ACAAAAAAAAT CAGCAACATC CGGACACTGC
701 TGCCCGTGGT GGAACAAGTG GCGAAAGCCA GCGCCCGCT GTTGATTATC
751 GCTGAAGACG TAGAAGGCAG AGCCTTGGCG ACTTTGGTCG TGAACAAACAT
801 CCGCGGCATC CTGAAAACCG TTGCGCTCAA AGCcccggc tTCGGcGACC
851 GCCGCAAAGC GATgtcgaa gaCATCGCCA TCCTGACCG cgccgTagtG
901 ATTtccGAAG Aagtccggc GTCTTTGGAA AAAAgcactT TGacgaCTT
951 Gggtaaaaaa acACGcatCG AAATCGGtga agaaaaaact ACCGTCACTcg
1001 acgGCTTCGG CGACCGcagc CAAAtcgaaag cgCGTGTGCG CGAAATCCGC
1051 CAACAAATCG AAACCGCGAC CAGCGATTAC GACAAAGAAA AACTGCAAGA
1101 GCGCGTTGCC AAACCTGGCAG GAGGCGTGGC AGTGATCAAA GTCGGCGCG
1151 CGACCGAAAGT CGAAATGAAA GAGAAAAAAAG ACCCGCTGGA AGACGCGCTG
1201 CACGCTACCC GCGCAGCCGT TGAAGAAGGC GTGGTTGCAG GCGCGGGCGT
1251 AGCCCTGTTG CGCGCCCGTG CCGCTTGGAA AAACCTGCAC ACCGGCAATG
1301 CCGACCAAGA CGCAGGCGTA CAAATCGTAT TGCGCGCCGT TGAGTCTCCG
1351 CTGCGCCAAA TCGBTGCCAA CGCAGGCGGA GAACCCAGCG TGTTGGTGAA
1401 CAAAGTGTG GAAGGCAAAG GCAactacgg TTACAAACGCa ggctcCGGCG
1451 AATACGgcga CATGATCGGA ATGGGCCTGC TCGACCCCTGC CAAAGTAACC
1501 CGTTCCGCGC TGCAACACGC CGCGTCTATC GCCGGTCTGA TGCTGACGAC
1551 CGACTGCATG ATTGCCGAAA TCCCTGAAGA AAAACCGCT GTGCCCGATA
1601 TGGGGGAAT GGGCGGTATG GGCAGCATGA TGTA

```

This corresponds to the amino acid sequence <SEQ ID 2962; ORF 982.ng>:

g982.pep

```

1 IASQNLRFDN RFLOKMVNGV NILPAADWVA LGAKGRNVVV DRAFGGPHIT
51 KDGVTVAKEI ELKDKFENMG AQMVKEVASK TNDVAGDGT TATVLAQSIV
101 AEGMKYVTAG MNPTDLKRGI DKAVAALVEE LKNIAKPCDT SKEIAQVGSI
151 SANSDEQVGA IIIAEAMEKVG KEVITVEDG KSLENELDVV EGMQFDRGYL
201 SPYFINDAEK QIAGLDNPFV LLFDKKISNI RDLLPVLEQV AKASRPLLII
251 AEDVEGEALA TLVVNNIRGI LKTVAVKAPG FGDRRKAMLQ DIAILTGGVV
301 ISEEVGLSLE KATLDDLQQT KRIEIGEENT TVIDFGDAA QIEARVAEIR
351 QQIETATSDY DKEKLQERVA KLAGGVAVIK VGAATEVEMK EKKDRVEDAL
401 HATRAAVEEG VVAGGGVALL RARAALENLH TGNADQDAGV QIVLRAVESP
451 LRQIVANAGG EPSVVVNKVL EGKGNYGYNA GSGEYGDMIG MGVLDPAKVT
501 RSALQHAASI AGLMLTTDCM IAEIPEEKPA VPDMGGMMG GGMM*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2963>:

m982.seq

```

1 ATGGCAGCAA AAGACGTACA GTTCGGCAAT GAAGTCCGTC AAAAAATGGT
51 AAACGGCGTG AACATTCTGG CAAACGCCGT CGCGTAACC TTGGGCCCA
101 AAGGTCGCAA CGTAGTCGTT GACCGCGCAT TCGGCCGCCGCACATCACC
151 AAAGACGGCG TAACCGTCGC CAAAGAAATC GAACTGAAAG ACAAGTTGA
201 AAATATGGGC GCGCAAATGG TGAAAGAAGT TCGGTCCAAA ACCAACGACG
251 TGGCAGGCGA CGGTACGACT ACCGCCACCG TACTGGCGCA ATCCATCGTT
301 GCCGAAGGTA TGAAATATGT TACCGCAGGT ATGAATCCGA CCGACCTGAA
351 ACGCGGTATC GATAAAGCCG TCGCCGCTTT GGTTGACGAA CTGAAAAAAC
401 TCGCCAAACCT TTGCGACACT TCTAAAGAAA TCGCCCCAGT CGGCTCTATT
451 TCCGCCAAACT CCGACGAACA AGTCGGCGCG ATTATCGCCG AAGCGATGGA
501 AAAAGTCGGC AAAGAAGGCG TGATTACCGT TGAAGACGGC AAGTCTTG
551 AAAACGAGCT GGACGTAGTT GAAGGTATGC AGTTCGACCG CGGCTACCTG
601 TCTCCTTACT TCATCAACGA TCGGGAAAAA CAAATCGCTG CTTGGACAA

```

651	TCCGTTTGT	TTGTTGTCG	ACAAAAAAAT	CAGCAACATC	CGCGACCTGC
701	TGCCTGTT	GGAACAAGTG	GCAAAAGCCA	GCCGTCGCT	TTGATTATC
751	GCTGAAGACG	TAGAAGGCGA	AGCCTTGGCG	ACTTTGGTCG	TGAACAAACAT
801	CCGAGGCATC	CTGAAAACCG	TTGCCGTCAA	AGCCCCCTGGC	TTCGGCAGACC
851	GCCCCAAAGC	GATGTTGCAA	GACATCGCCA	TCCTGACCAGG	CGCGTGGTG
901	ATTTCCGAAG	AAGTCGGTCT	GTCTTGGAA	AAAGCGACTT	TGGACGACTT
951	GGGTCAAGCC	AAACGCATCG	AAATCGGTAA	AGAAAAACACC	ACCATCATCG
1001	ACGGCTTGG	CGACGCAGCC	CAAATCGAAG	CGCGTGTG	CGAAATCCGC
1051	CAACAAATCG	AAACCGCAAC	CAGCGATTAC	GACAAAAGAAA	AACTGCAAGA
1101	GCGCGTGGCT	AAATTGGCAG	GCGGCGTGGC	AGTCATCAAA	GTGGTGTGCC
1151	CGACCGAAGT	CGAAATGAAA	GAGAAAAAAAG	ACCGCGTGG	AGACCGCGCTG
1201	CACGCTACCC	GCGCAGCCGT	TGAAGAAGGC	GTGGTGCAG	GCGGCGGCGT
1251	AGCCCTGTT	CGTGCCTGTG	CTGCTTGGG	AAACCTGCAC	ACCGGCAATG
1301	CCGACCAAGA	CGCAGCGTA	CAAATCGTCT	TGCGCGCCGT	TGAGTCTCCG
1351	CTGCGCCAAA	TCGTTGCCA	CGCAGGCGGC	GAACCCAGCG	TGGTTGTGAA
1401	CAAAGTATTG	GAAGGCAAAG	GCAACTACGG	TTACAACGCT	GGCAGCGGCG
1451	AATACTGGCA	TATGATCGAA	ATGGGCGTAC	TCGACCCCGC	CAAAGTAACC
1501	CGTTCTGCGC	TGCAACACGC	CGCATCTATC	TGGCGCTTGA	TGCTGACCAC
1551	TGATTGCATG	ATCGCTGAAA	TCCCCGAAGA	CAAACGGCT	GTGCGCTGATA
1601	TGGGCGGGCAT	GGGTGGTATG	GGCGGCATGA	TGTAA	

This corresponds to the amino acid sequence <SEO ID 2964: ORF 982>:

m982.sea

1	ATGGCAGCAA	AAGACGTACA	GTTCGGCAAT	GAAGTCGTC	AAAAAAATGGT
51	AAACGGCGTG	AACATTCTGG	CAAACGCCGT	CCGCCTAACCC	TTGGGCCCCA
101	AAGGTGCGAA	CGTAGTCGTT	GACC CGCGCAT	T CGCGGGCCC	GCACATCACC
151	AAAGACGGCG	TAACC GTCGC	CAAAGAAATC	GAACTGAAAG	ACAAGTTGAA
201	AAATATGGC	GCGCAAATGG	TGAAAGAAGT	TGCGTCCAAA	ACCAACGACG
251	TGGCAGGGCA	CGGTACGACT	ACCGGCCACCG	TACTGGCGCA	ATCCATCGTT
301	GCCCAGGTTA	TGAAATATGT	TACCGCAGGT	ATGAATCCGA	CCGACCTGAA
351	ACGCGGTATC	GATAAAAGCCG	TGCGCGCTTT	GGTTGACGAA	CTGAAAAAACAA
401	TGCGCAAAAC	TTGCGACACT	TCTAAAGAAA	TCGCCAAGT	CGGCTCTATT
451	TCCGCCAAC	CCGACGAACA	AGTCGGCGCG	ATTATCGCCG	AAGCGATGGA
501	AAAAGTCGGC	AAAGAAGGCG	TGATTACCGT	TGAAGACGGC	AAGCTTTGG
551	AAAACGAGCT	GGACGTAGTT	GAAGGTATGC	AGTTGACCGG	CGGCTACCTG
601	TCTCCTTACT	TCATCAACGA	TGCGGAAAAAA	CAAATCGCTG	CTTGGACACAT
651	TCCGTTTGT	TTGTTGTCG	ACAAAAAAAT	CAGCAACATC	CGGACCTGCG
701	TGCCCTGTTT	GGAAACAAGT	GCAAAAGCCA	GCCGTCCGCT	GTTGATTATC
751	GCTGAAGACG	TAGAAGGCGA	AGCCTTGGCG	ACTTTGGTCG	TGAAACAACAT
801	CCGAGGCATC	CTGAAAACCG	TTGCGTCAA	AGCCCCCTGGC	TTGGCGACCC
851	CGCCGAAAGC	GATGTGCAA	GACATCGCCA	TCCTGACCGG	CGGCGTGGTG
901	ATTTCCGAA	AAGTCGGTCT	GTCTTTGGAA	AAAGCGACTT	TGGACGACTT
951	GGGTCAAGCC	AAACGCATCG	AAATCGGTAA	AGAAAACACC	ACCATCATCG
1001	ACGGCTTGG	CGACGCGACC	CAAATCGGA	CGCGTGTG	CGAAATCCGC
1051	CAACAAATCG	AAACCGCAAC	CAGCGATTAC	GACAAAGAAA	AACTGCAAGA
1101	GGCGTGGCT	AAATTGGCAG	GGCGCGTGGC	AGTCATCAA	FTGGGTGCGCG
1151	CGACCGAAGT	CGAAATGAAA	GAGAAAAAAAG	ACCGCGTGG	AGACCGCGCTG
1201	CACGCTACCC	GCGCAGCCGT	TGAAGAAGGC	GTGGTTGCAG	CGGGCGGGCGT
1251	AGCCCTGTTG	CGTGCCTCGT	CTGCTTTGGA	AAACCTGCAC	ACCGGCAATG
1301	CCGACCAAGA	CGCAGCGTA	CAAATCGTCT	TGCGCCCGT	TGAGTCTCCG
1351	CTGCGCCAAA	TCGTTGCCAA	CGCAGCGGGC	GAACCCACCG	TGTTGTTGAA
1401	CAAAGTATTG	GAAGGCAAAAG	GCAACTACCG	TTACAACCGT	GGCAGCGCG
1451	AATAACGGCA	TATGATCGAA	ATGGGCGTAC	T CGCACCCCG	CAAAGTAACC
1501	CGTTCTGCGC	TGCAACACGC	CGCACATCTATC	T GCGGCTTGA	TGCTGACCAC
1551	TGATTGCATG	ATCGCTGAAA	TCCCCGAAGA	CAAACCGGCT	GTGCGCTGATA
1601	TGGGCGGGCAT	GGGTGGTATG	GGCGGCATGA	TGTAA	

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m982/g982 95.8% identity in 544 aa overlap

m982.pep	10	20	30	40	50	60
	MAAKDVFQFGNEVRQKMVN	G	V	N	I	A
	ILANAVRVT	L	G	P	K	R
	LGPKGRNVV	V	D	R	A	F
	V	V	V	G	G	G
	D	R	A	F	G	P
	V	V	V	G	H	I
	A	E	K	I	T	K
	V	A	K	E	D	G
	K	E	I	K	V	T

g982	IASQNLRFDNRFLQKMQVNGVNILPAADWVALGAKGRNVVVDRAGGGPHITKGTVAKEI					
	10	20	30	40	50	60
m982.pep	70	80	90	100	110	120
	ELKDKFENMGAQMVKVEASKTNDVAGDGTATVLAQSIVAEGMKYVTAGMNPTDLKRGI					
g982	70	80	90	100	110	120
	ELKDKFENMGAQMVKVEASKTNDVAGDGTATVLAQSIVAEGMKYVTAGMNPTDLKRGI					
m982.pep	130	140	150	160	170	180
	DKAVAALVDELKNIAKPCDTSKEIAQVGSIANSDEQVGAIIEAMEKVGKEGVITVEDG					
g982	130	140	150	160	170	180
	DKAVAALVEELKNIAKPCDTSKEIAQVGSIANSDEQVGAIIEAMEKVGKEGVITVEDG					
m982.pep	190	200	210	220	230	240
	KSLENELDVVEGMQFDRGYLSFYFINDAEKQIAALDNPVLLFDKKISNIRDLLPVLEQV					
g982	190	200	210	220	230	240
	KSLENELDVVEGMQFDRGYLSFYFINDAEKQIAGLDNPVLLFDKKISNIRDLLPVLEQV					
m982.pep	250	260	270	280	290	300
	AKASRPLLIIAEDVEGEALATLVNNIRGILKTVAVKAPGFGDRRKAMLQDIAILTGGVV					
g982	250	260	270	280	290	300
	AKASRPLLIIAEDVEGEALATLVNNIRGILKTVAVKAPGFGDRRKAMLQDIAILTGGVV					
m982.pep	310	320	330	340	350	360
	ISEEVGLSLEKATLDDLGQAKRIEIGKENTTIIDGFQDAAQIEARVAEIRQQIETATSDY					
g982	310	320	330	340	350	360
	ISEEVGLSLEKATLDDLGQTKRIEIGEENTTVIDGFQDAAQIEARVAEIRQQIETATSDY					
m982.pep	370	380	390	400	410	420
	DKEKLQERVAKLAGGVAVIKVGAATEEVEMKEKKDRVEDALHATRAAVEEGVVAGGGVALL					
g982	370	380	390	400	410	420
	DKEKLQERVAKLAGGVAVIKVGAATEEVEMKEKKDRVEDALHATRAAVEEGVVAGGGVALL					
m982.pep	430	440	450	460	470	480
	RARAALENLHTGNADQDAGVQIVLRAVESPLRQIVANAGGEPSVSVNKVLEGKGNYGYNA					
g982	430	440	450	460	470	480
	RARAALENLHTGNADQDAGVQIVLRAVESPLRQIVANAGGEPSVSVNKVLEGKGNYGYNA					
m982.pep	490	500	510	520	530	540
	GSGEYGDMIEMGVLDPAKVTRSLQHAAASIAGLMLTDCMIAEIPEKDPAVPDMGGMGGM					
g982	490	500	510	520	530	540
	GSGEYGDMIGMGVLDPAKVTRSLQHAAASIAGLMLTDCMIAEIPEEKPAVPDMGGMGGM					
m982.pep	GGMMX					
g982						

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2965>:
a982.seq

1	ATGGCAGCAA	AAGACGTACA	ATTGGCAAT	GAAGTCCGCC	AAAAAATGGT
51	AAACGGCGTG	AACATTGG	CAAACGCCGT	GCGCGTAACC	TTGGGTCCCA
101	AAGGCCGCAA	CGTGGTGGTT	GACCGCGCTT	TGGCGGCC	GCACATCACC
151	AAAGACGGCG	TAACCGTCGC	CAAAGAAATC	GAACTGAAAG	ACAAGTTGA
201	AAATATGGGC	GCGCAAATGG	TGAAAGAAGT	CGCGTCCAAA	ACCAACGACG
251	TGGCGGGCGA	CGGTACGACT	ACCGCCACCG	TATTGGCGCA	ATCCATCGTT
301	GCCGAAGGTA	TGAAATACGT	TACCGCCGGT	ATGAACCCGA	CCGACCTGAA
351	ACGCGGTATC	GACAAAGCCG	TCGCCGCTTT	GGTTGAAGAG	CTGAAAACA

401 TCGCCAAACC TTGCGACACT TCTAAAGAAA TCGCCAAGT CGGCTCTATT
 451 TCCGCCAACT CTGACGAACA AGTCGGCGCG ATTATTGCCG AAGCGATGGA
 501 AAAAGTCGGC AAAGAAGGCG TGATTACCGT TGAAGACGGC AAATCTTG
 551 AAAACGAGCT GGACGTGGTT GAAGGTATGC AATTGACCG CGGCTACCTG
 601 TCTCCTTACT TCATCAACGA TGCGGAAAAA CAAATCGCCG GCTTGGACAA
 651 TCCGTTGTA TTGCTGTTG ACAAAAAAAT CAGCAATATC CGCGACCTGC
 701 TGCCTGTTT GGAACAAGTG GCCAAAGCCA GCCGTCGCT GTTGATTATC
 751 GCTGAAGACG TAGAAGGCGA AGCCTGGCG ACTTTGGTCG TGAACAAACAT
 801 CGCGGGCATT CTGAAAACCG TTGCCGTTAA AGCTCCGGGC TTCGGCGACC
 851 GCCGCAAAGC GATGCTGCAA GACATCGCTA TCCTGACCGG CGGCACAGTG
 901 ATTTCCGAAG AAGTCGGCCT GTCTTGGAA AAAGCGACTT TGAGACGACTT
 951 GGGTCAGGCC AAACGCATCG AAATCGGTA AGAAAACACC ACCATCATCG
 1001 ACGGCTTCGG CGACGCAGCC CAAATCGAAG CGCGTGTGCG CGAAATCCGC
 1051 CAACAAATCG AAACCGCAAC CAGCGATTAC GACAAAGAAA AACTGCAAGA
 1101 GCGCGTTGCC AAACCGAGC GCGGCCTGGC AGTAATCAAA GTCGGTGC
 1151 CGACCGAAGT GGAAATGAAA GAGAAAAAAAG ACCCGCTGGA AGACCGCCTG
 1201 CACGCTACCC GCGCAGCCGT TGAAGAAGGC GTGGTGCAG GCGGCGGC
 1251 AGCCCTGTT CGCGCCCGTG CGCGCTCGGA AAACCTGCAC ACCGGCAATG
 1301 CAGACCAAGA CGCAGCGTA CAAATCGCT TGCGCCCGT TGAGTCTCCG
 1351 CTGCGCCAAA TCGTTGCCAA CGCAGCGGGC GAACCCAGCG TGTTGTGAA
 1401 CAAAGTGTG GAAGGCAAAG GCAACTATGG TTACAAACGCT GGCAGCGGC
 1451 AATACGGCGA CATGATCGAA ATGGGCGTAC TCGACCCGC CAAAGTAACC
 1501 CGTTCCGCGC TGCAACACGC CGCGCTATC GCCGGCTGA TGCTGACCAC
 1551 AGACTGCATG ATTGCTGAAA TCCCTGAAGA CAAACCGCT ATGCCTGATA
 1601 TGGCGGGCAT GGGTGGTATG GGCAGCGATGA TGTAA

This corresponds to the amino acid sequence <SEQ ID 2966; ORF 982.a>:

a982.pep

1 MAAKDQVQFGN EVRQKMNVG NILANAVRVTLGPKGRNVVV DRAFGGPHIT
 51 KDGVTVAKEI ELKDKFENMG AQMVKEVASK TNDVAGDGT TATVLAQSIV
 101 AEGMKYVTAG MNPTDLKRGI DKAVAALVEE LKNIAKPCDT SKEIAQVGSI
 151 SANSDEQVGA IIAEAMEKVG KEGVITVEDG KSLENELDV EGMQFDRGYL
 201 SPYFINDAEK QIAGLDNPFV LLFDKKISNI RDLLPVLEQV AKASRPLLII
 251 AEDVEGEALA TLVNNIRGI LKTVAVKAPG FGDRRKAMLQ DIAILTGGTV
 301 ISEEVGLSLE KATLDDLQGA KRIEIGKENT TIIDGFDAA QIEARVAEIR
 351 QQIETATSDY DKEKLQERVA KLAGGVAVIK VGAATEVEMK EKKDRVEDAL
 401 HATRAAVEEG VVAGGGVALL RARAALENLH TGNADQDAGV QIVLRAVESP
 451 LRQIVANAGG EPSVVVNKL EGKGNYGYNA GSGEYGDME MGVLDPAKVT
 501 RSALQHAASI AGMLTTDCM IAEIPEDKPA MPDMGGMM GGMM*

m982/a982 99.3% identity in 544 aa overlap

	10	20	30	40	50	60
m982.pep	MAAKDVQFGNEVRQKMNVGNILANAVRVTLGPKGRNVVV DRAFGGPHIT KDGVTVAKEI					
a982	MAAKDVQFGNEVRQKMNVGNILANAVRVTLGPKGRNVVV DRAFGGPHIT KDGVTVAKEI	10	20	30	40	50
		70	80	90	100	110
m982.pep	ELKDKFENMG AQMVKEVASK TNDVAGDGT TATVLAQSIV AEGMKYVTAG MNPTDLKRGI					
a982	ELKDKFENMG AQMVKEVASK TNDVAGDGT TATVLAQSIV AEGMKYVTAG MNPTDLKRGI	70	80	90	100	110
		120				
m982.pep	DKAVAALVDELKNIAKPCDT SKEIAQVGSI SANSDEQVGAI IAEAMEKVG KEGVITVEDG	130	140	150	160	170
a982	DKAVAALVEELKNIAKPCDT SKEIAQVGSI SANSDEQVGAI IAEAMEKVG KEGVITVEDG	130	140	150	160	170
		180				
m982.pep	KSLNELDVVEGMQFDRGYLSPYFINDAEKQIAALDNPVLLFDKKISNIRDLLPVLEQV	190	200	210	220	230
a982	KSLNELDVVEGMQFDRGYLSPYFINDAEKQIAALDNPVLLFDKKISNIRDLLPVLEQV	190	200	210	220	230
		240				

	250	260	270	280	290	300
m982.pep	AKASRPLLIIAEDVEGEALATLVVNNIRGILKTVAVKAPGFGDRRKAMLQDIAILTGGVV : : : : : : : : : : : :					
a982	AKASRPLLIIAEDVEGEALATLVVNNIRGILKTVAVKAPGFGDRRKAMLQDIAILTGGTV 250 260 270 280 290 300					
	310	320	330	340	350	360
m982.pep	ISEEVGLSLEKATLDDLQAKRIEIGKENTTIIDGFGDAAQIEARVAEIRQQIETATSDY : : : : : : : : : : : : :					
a982	ISEEVGLSLEKATLDDLQAKRIEIGKENTTIIDGFGDAAQIEARVAEIRQQIETATSDY 310 320 330 340 350 360					
	370	380	390	400	410	420
m982.pep	DKEKLQERVAKLAGGVAVIKVGAATEVEMKEKKDRVEDALHATRAAVEEGVVAGGGVALL : : : : : : : : : : : : :					
a982	DKEKLQERVAKLAGGVAVIKVGAATEVEMKEKKDRVEDALHATRAAVEEGVVAGGGVALL 370 380 390 400 410 420					
	430	440	450	460	470	480
m982.pep	RARAALENLHTGNADQDAGVQIVLRAVESPLRQIVANAGGEPSVVVNKVLEGKGNYGYN : : : : : : : : : : : :					
a982	RARAALENLHTGNADQDAGVQIVLRAVESPLRQIVANAGGEPSVVVNKVLEGKGNYGYN 430 440 450 460 470 480					
	490	500	510	520	530	540
m982.pep	GSGEYGDIMIEMGVLDPAKVTRSALQHAASIAGLMLTDCMIAEIPEDKPAVPDMGGMGM : : : : : : : : : : :					
a982	GSGEYGDIMIEMGVLDPAKVTRSALQHAASIAGLMLTDCMIAEIPEDKPAMPDMGGMGM 490 500 510 520 530 540					
m982.pep	GGMMX 					
a982	GGMMX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2967>:

g986.seq	1	GTGTTCAAAA	AATACCAATA	CTTCGCTTTG	GCGGCACTGT	GTGCCGCC
	51	GCTGGCAGGGC	TGCGAAAAGG	CAGGCAGCTT	TTTCGGTGCG	GACAAAAAAG
	101	AAGCATCCTT	CGTAGAACACG	ATCGAACACA	CCAAAGACGA	CGGCAGTGTC
	151	AGTATGCTGC	TGCCCCACTT	TGCCCCACTG	GTTCAAAGCG	AAGGCCCAGG
	201	AGTCGTCAAT	ATTCAAGGCAG	CCCCCGCCCC	CGGCACCCAA	AACGGCAGCG
	251	GCAATGCCGA	AACCAGATTCC	GACCCGCTTG	CCGACAGCGA	CCCGTTCTAC
	301	GAATTTTCA	AACGCCCTCGT	CCCGAACATG	CCCGAAATCC	CCCAAGAAGA
	351	AGCAGATGAC	GGCGGATTGA	ACTTCGGTT	GGGCTTCATC	ATCAGCAAAA
	401	ACGGCTACAT	CCTGACCAAT	ACCCACGTG	TTGCCGGTAT	GGGCAGTATC
	451	AAAGTCTTCG	TCAACGACAA	GCGCGAATAT	ACCGCCAAAC	TCATCGGTT
	501	GGATGTCCAA	TCCGATGTG	CCCTCTGAA	AATCGACGCA	ACGGAAGAGC
	551	TACCCGTCGT	CAAATCGGC	AATCCCCAAA	ATTGAAACC	GGGCGAATGG
	601	GTCGCTGCCA	TCGGCGCGCC	CTTCGGTT	GACAACAGCG	TGACCGCCGG
	651	CATCGTGTCC	CGAACAAAGGA	GAAGCCTGCG	CAACGAAAGc	tACACACCC
	701	TCATCCAAAC	CGACGTTGCC	ATCAATCCG	GCAATTCCGG	CGGCCCCGCTG
	751	TTCAACTTAA	AAGGACAGGT	cgtCGGCATC	AATTGCGAAA	TATACAGCCG
	801	CAGCGgggaa	ttCATGGGCA	TCTCCTTTGC	CATCCCGATT	GACGTTGCCA
	851	TGAATGTGCG	CGAACAGCTG	AAAAACACCG	GCAAAGTCCA	ACGGGGACAA
	901	CTGGGCGTGA	TTATTCAAGGA	AGTATCCTAC	GGTTTGGCAC	AGTCGTT
	951	TCTGGATAAA	GCCAGCGCG	CATTGATTGC	CAAATCCTT	CCCGGCAGCC
	1001	CCGCAGAACG	TGCCGGCCTG	CAGGCGGGCG	ACATCGTCC	CAGCCTCGAC
	1051	GGCGGAGAAA	TACGTCTTC	CGGGCACCTT	CCCGTCATGG	TCGGCGCCAT
	1101	TACGCCGGGA	AAAGAACGTCA	GCTCTGGCGT	ATGGCGAAA	GGCGAAGAAA
	1151	TCACAATCAA	AGCCAAGCTG	GGCAACGCC	ccgagcatac	CGGCGcatCA
	1201	TCCAAAACAG	ATGAAgcccc	ctacaccgAA	CAGCAATCCG	GTACGTTCTC
	1251	GGTCGAATCC	GCAGGCATTA	CCCTTCAGAC	ACATACCGAC	AGCAGCGGca
	1301	aacacctcg	cgtcgtaacgg	gttccgacg	cggcagaacg	cGCAGGCTTA

1351 AGgcgcggcg acgaaatcct cgcggcggg caagtccccg tcaatgacga
 1401 agccgGTTTC cgcaaaGCTA TGGACAAGGC AGGAAAAAC GTCCCCCTGC
 1451 TGGTCATgcg ccgTGGCAAC ACGCTGTTCA TCGCATTAAA CCTGCAATAA

This corresponds to the amino acid sequence <SEQ ID 2968; ORF 986.ng>:

g986.pep

1 VFKKYQYFAL AALCAALLAG CEKAGSFFGA DKKEASFVER IEHTKDDGSV
 51 SMLLPDFAQL VQSEGPVVN IQAAPAPRTQ NGSGNAETDS DPLADSDPFY
 101 EFFKRLVPNM PEIPQEEADD GGLNFGSGFI ISKNGYILTN THVVAGMGSI
 151 KVLLNDKREY TAKLIGSDVQ SDVALLKIDA TEELPVVKIG NPKNLKPGEW
 201 VAAIGAPFGF DNSVTAGIVS AKGRSLPNES YTPFIQTDVA INPGNSGGPL
 251 FNLKGQVVGI NSQIYSRSGG FMGISFAIPI DVAMNVAEQL KNTGKVQRGQ
 301 LGVIIQEVSY GLAQSFGLDK AGGALIAKIL PGSPAERAGL QAGDIVLSLD
 351 GGEIRSSGDL PVMVGAITPG KEVSLGVWRK GEEITIKAKL GNAAEHTGAS
 401 SKTDEAPYTE QOSGTFSVES AGITLQTHTD SSGGHLVVVR VSDAAERAGL
 451 RRGDEILAVG QVPVNDEAGF RKAMDAGKN VPLLIMRRGN TLFIALNLQ*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2969>:

m986.seq

1 GTGTTCAAAA AATACCAATA CCTCGCTTTG GCAGCACTGT GTGCAGCCTC
 51 GCTGGCAGGC TGCGACAAGG CAGGCAGCTT CTTCTGGCG GACAAAAAAG
 101 AACCATCCTT CGTAGAACCGC ATCGAACACA CCAAAGACGA CGGCAGCGTC
 151 AGTATGCTGC TGCCCAACTG GTTCAAAGTG AAGGTCCGGC
 201 AGTCGTCAAT ATTCAAGGCAG CCCCCGCCCGC GCGCACCAA AACGGCAGCG
 251 GCAATGCCGA AAACGATTCC GACCCGATTG CCGACAAACG CCGTTCTAC
 301 GAATTTTCA AACGCCCTCGT CCCGAATATG CCCGAATTC CCCAAGAAGA
 351 AGCAGATGAC GGCAGATTGA ACTTCGGTTG GGGCTTCATC ATCAGCAAAG
 401 ACGGCTACAT CCTGACCAAT ACCCACGTC TTACCGGCAT GGGCAGTATC
 451 AAAGTCTGC TCAACGACAA GCGCGAATAT ACCGCCAAC TCATCGGTTTC
 501 GGATGTCAA TCCGATGTGCG CCCTCTGAA AATCGACGCA ACGGAAGAGC
 551 TGCCCCTCGT CAAAATCGGC AATCCAAAG ATTTGAAACC GGGCGAATGG
 601 GTCGCCGCCA TCAGCGCGCC CTTCCGGCTTC GACAACAGCG TGACCGCCGG
 651 CATCGTGTCC GCCAAGGCA GAAGCCTGCG CAACGAAAGC TACACACCCCT
 701 TCATCCAAAC CGACGTTGCC ATCAATCCGG GCAACTCCGG CGGCCCGCTG
 751 TTCAACTTAA AAGGACAGGT CGTCGGCATC AACTCGCAA TATACAGCCG
 801 CAGCGCGGA TTCATGGCA TTCCCTTCG CATCCCGATT GACGTTGCCA
 851 TGAATGTCG CCGAACAGCTG AAAAACACCG GCAAAGTCCA ACGCGGACAA
 901 CTGGCGTGA TTATTAAGA AGTATCCTAC GGTTTGGCAC AATCGTTGG
 951 TTTGGACAAA GCGGGCGCG CACTGATTGC CAAAATCTG CGCCGCAGCC
 1001 CCGCAGAACG TGCCGGCTG CAGGCGGGCG ACATCGCTC CAGCCTCGAC
 1051 GGCAGGAGAAA TACGTTCTTC CGGCGACCTT CCCGTTATGG TCGCGGCCAT
 1101 TACGCCGGGA AAAGAAGTC GAACGCGCTG ATGGCGAAA GCGGAAGAAA
 1151 TCACAATCAA AGTCAAGCTG GCGAACGCGC CCGAGCATAT CGGGCGCATCA
 1201 TCCAAAACAG ATGAAGCCCC CTACACCGA CAGCAATCCG GTACGTTCTC
 1251 GGTCAAGATCC GCAGGGCATTA CCCTTCAGAC ACATACCGAC AGCAGCGCG
 1301 GACACCTCGT CGTCGTACGG GTTCCCGACG CGCAGAACG CGCAGGCTTG
 1351 AGGCGCGGGC AGCAGATTCT TGCGCTCGGG CAAGTCCCCG TCAATGACGA
 1401 AGCCGGTTTC CGCAAAGCTA TGACACAAGGC AGGAAAAAC GTCCCCCTGC
 1451 TGATCATGCG CGCTGGCAAC ACGCTGTTA TCGCATTAAA CCTGCAATAA

This corresponds to the amino acid sequence <SEQ ID 2970; ORF 986>:

m986.pep..

1 VFKKYQYLAL AALCAASLAG CDKAGSFFVA DKKEASFVER IEHTKDDGSV
 51 SMLLPDFAQL VQSEGPVVN IQAAPAPRTQ NGSGNAENDS DPLADNDPFY
 101 EFFKRLVPNM PEIPQEEADD GGLNFGSGFI ISKDGYILTN THVVAGMGSI
 151 KVLLNDKREY TAKLIGSDVQ SDVALLKIDA TEELPVVKIG NPKNLKPGEW
 201 VAAIGAPFGF DNSVTAGIVS AKGRSLPNES YTPFIQTDVA INPGNSGGPL
 251 FNLKGQVVGI NSQIYSRSGG FMGISFAIPI DVAMNVAEQL KNTGKVQRGQ
 301 LGVIIQEVSY GLAQSFGLDK AGGALIAKIL PGSPAERAGL QAGDIVLSLD
 351 GGEIRSSGDL PVMVGAITPG KEVSLGVWRK GEEITIKVNL GNAAEHIGAS
 401 SKTDEAPYTE QOSGTFSVES AGITLQTHTD SSGGHLVVVR VSDAAERAGL
 451 RRGDEILAVG QVPVNDEAGF RKAMDAGKN VPLLIMRRGN TLFIALNLQ*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m986/g986 97.0% identity in 499 aa overlap

	10	20	30	40	50	60
m986.pep	VFKKYQYLALAALCAASLAGCDKAGSFFVADKKEASFVERIEHTKDDGSVSMLLPDAQL					
g986	: : : : : : : : : :					
	VFKKYQYFALAALCAALLAGCEKAGSFFGADKKEASFVERIEHTKDDGSVSMLLPDAQL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m986.pep	VQSEGPBVNIQAAAPAPRTQNGSGNAENDSDPIADNDPFYEFFKRLVPNMPEIPQEEADD					
g986	: : : : : : : : : :					
	VQSEGPBVNIQAAAPAPRTQNGSGNAETDSDPLADSDPFYEFFKRLVPNMPEIPQEEADD					
	70	80	90	100	110	120
	130	140	150	160	170	180
m986.pep	GGLNFGSGFIISKDGYILTNTHVVTGMGSIKVLLNDKREYTAKLIGSDVQSDVALLKIDA					
g986	: : : : : : : : : :					
	GGLNFGSGFIISKNGYILTNTHVVAAGMGSIKVLLNDKREYTAKLIGSDVQSDVALLKIDA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m986.pep	TEELPVVKIGNPKDLKPGEWVAAIGAPFGFDNSVTAGIVSAKGRSLPNESYTPFIQTDVA					
g986	: : : : : : : : : :					
	TEELPVVKIGNPKNLKPGEWVAAIGAPFGFDNSVTAGIVSAKGRSLPNESYTPFIQTDVA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m986.pep	INPGNSGGPLFNLKGQVVGINSQIYSRSGGFMGISFAIPIDVAMNVAEQLNTGKVQRGQ					
g986	: : : : : : : : : :					
	INPGNSGGPLFNLKGQVVGINSQIYSRSGGFMGISFAIPIDVAMNVAEQLNTGKVQRGQ					
	250	260	270	280	290	300

m986.pep	310	320	330	340	350	360
	LGVIIQEVSYGLAQSFGLDKAGGALIAKILPGSPAERAGLQAGDIVLSLDGGEIRSSGDL					
g986	310	320	330	340	350	360
	LGVIIQEVSYGLAQSFGLDKASGALIAKILPGSPAERAGLQAGDIVLSLDGGEIRSSGDL					
m986.pep	370	380	390	400	410	420
	PVMVGAITPGKEVSLGVWRKGEETIKVKGNAEHIGASSKTDEAPYTEQQSGTFSVES					
g986	370	380	390	400	410	420
	PVMVGAITPGKEVSLGVWRKGEETIKAKLGNAEHTGASSKTDEAPYTEQQSGTFSVES					
m986.pep	430	440	450	460	470	480
	AGITLQTHTDSSGGHLVVVRVSDAAERAGLRRGDEILAVGQVPVNDEAGFRKAMDAGKN					
g986	430	440	450	460	470	480
	AGITLQTHTDSSGKHLVVVRVSDAAERAGLRRGDEILAVGQVPVNDEAGFRKAMDAGKN					
m986.pep	490	500				
	VPLLIMRRGNTLFIALNLQX					
g986	490	500				
	VPLLVMRRGNTLFIALNLQX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2971>:

a986.seq

```

1 GTGTTCAAAA AATACCAATA CCTCGCTTG GCAGCACTGT GTGCCGCCTC
51 GCTGGCAGGC TGCGACAAAG CCGGCAGCTT TTTCGGTGCG GACAAAAAAG
101 AAGCATCCTT TGTAGAACGC ATCAAACACA CCAAAGACGA CGGCAGCGTC
151 AGTATGCTGC TGCCCGACTT TGTCCAACTG GTTCAAAGCG AAGGCCCGGC
201 AGTCGTCAAT ATTCAAGGCAG CCCCCGCCCA GCGCACCCAA AACGGCAGCA
251 GCAATGCCGA AACCGATTCC GACCCGCTTG CCGACAGCGA CCCGTTCTAC
301 GAATTTTCA AACGCCTCGT CCCGAACATG CCGAAATCC CCCAAGAAGA
351 AGCAGATGAC GGNGGATTGA ACTTCGGTTG GGGCTTCATC ATCAGCAAAG
401 ACGGCTATAAT TCTGACCAAT ACGCACGTG TTACCGGCAT GGGCAGTATC
451 AAAAGTCCCTGC TCAACGACAA CGCGAATAT ACCGCOAAAC TCATCGGTTTC
501 GGATGTCCAA TCCGATGTGCG CCCTTCTGAA AATCGACGCA ACGGAAGAGC
551 TGCCCGTCGT CAAAATCGGC AATCCCAAAG ATTGAAACC GGGCGAATGG
601 GTCGCCGCCA TCGGCGCGCC CTTCGGCTTC GACAACAGCG TGACCGCCGG
651 CNTCGTGTCC GCCAAAGGCA GAAGCCTGCC CAACGAAAGC TACACACCCCT
701 TCATCCAAAC CGACGTTGCC ATCAATCCGG GCAACTCCGG CGGCCCGCTG
751 TTCAACTTAA AAGGACAGGT CGTCGGCATC AACTCGCAAAT TATACAGCCG
801 CAGCGGCCGA TTCATGGCA CATCCCCTCG CATCCCAGT GACGTTGCCA
851 TGAATGTGCG CGAACAGCTG AAAAACACCG GCAAAGTCCA ACCGGGACAA
901 CTGGGCGTGA TTATTCAGA AGTATCCTAC GGTGGCAG AATCGTTCGG
951 TTTGGACAAA GCGGGCGCG CACTGATTGC CAAAATCCTG CCCGGCAGCC
1001 CCGCAGAACG TGCCGCCCTG CGGGCGGGCG ACATCGCTT CAGCTCGAC
1051 GGCAGGAGAAA TACGTTCTTC CGGCGACCTT CCCGTTATGG TCGGCCCAT
1101 TACGCCGGGA AAAGAAGTCA GCCTCGCGT ATGGCGAAA GGCAGAGAAA
1151 TCACAATCAA AGTCAAGCTG GGCACCGCC CCGAGCATAT CGGCGCATCA
1201 TCCAAAACAG ATGAAGCCCC CTACACCGA CAGCAATCCG GTACGTTCTC
1251 GGTGAAATCC GCAGGCGATTA CCCTTCAGAC ACATACCGAC AGCAGCGCG
1301 GACACCTCGT CGTCGTACGG GTTCCGACCG CGGCAGAACG CGCAGGCTTG
1351 AGGCGCGCG ACGAAATTCT TGGCGTCGGG CAAGTCCCCG TCAATGACGA
1401 AGCCGGTTTC CGCAAAGCTA TGGACAAGGC AGGCAAAAC GTCCCCCTGC
1451 TGATCATGCG CGCTGGCAAC ACGCTGTTA TCGCATTAAA CCTGCAATAA

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This corresponds to the amino acid sequence <SEQ ID 2972; ORF 986.a>:

a986.pep

```

1 VFKKYQYLAL AALCAASLAG CDKAGSFFGA DKKEASFVER IKHTKDDGSV
51 SMLLPDFVQL VQSEGPBVNV IOAAPAPRTO NGSSNAETDS DPLADSDPFY
101 EFFFKRLVPNM PEIPQEEADD GGLNFGSGFI ISKDGYILTN THVVTGMGSI
151 KVLLNDKREY TAKLIGSDVQ SDVALLKIDA TEELPVVKIG NPKDLKPGEW
201 VAAIGAPFGF DNSVTAGXVS AKGRSLPNES YTPFIQTDVA INPGNSGGPL
251 FNLKGQVVGQ NSQIYSRSGG FMGISFAIPI DVAMNVAEQL KNTGKVQRGQ

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301 LGVIIQEVSY GLAQSFGLDK AGGALIAKIL PGSPAERAGL RAGDIVLSLD
 351 GGEIRSSGDL PVMVGAITPG KEVSLGVWRK GEEITIKVKL GNAAEHIGAS
 401 SKTDEAPYTE QQSGTFSVES AGITLQTHTD SSGGHLVVVR VSDAAERAGL
 451 RRGDEILAVG QVPVNDEAGF RKAMDKAGKN VPLLIMRRGN TLFIALNLQ*

m986/a986 98.2% identity in 499 aa overlap

m986.pep	10	20	30	40	50	60
	VFKKYQYLALAALCAASLAGCDKAGSFFVADKKEASFVERIEHTKDDGSVSMLLPDFAQI					
a986	VFKKYQYLALAALCAASLAGCDKAGSFFGADKKEASFVERIKHTKDDGSVSMLLPDFVQL					
	10	20	30	40	50	60

m986.pep	70	80	90	100	110	120
	VQSEGPAAVNNIQAAPAPRTQNGSGNAENDSDPIADNDPFYEFFKRLVPNMPEIPQEEADD					
a986	VQSEGPAAVNNIQAAPAPRTQNGSSNAETSDPLADSDPFYEFFKRLVPNMPEIPQEEADD					
	70	80	90	100	110	120

m986.pep	130	140	150	160	170	180
	GGLNFSGFIISKDGYILTNTHVVVTGMGSIKVLLNDKREYTAKLIGSDVQSDVALLKIDA					
a986	GGLNFSGFIISKDGYILTNTHVVVTGMGSIKVLLNDKREYTAKLIGSDVQSDVALLKIDA					
	130	140	150	160	170	180

m986.pep	190	200	210	220	230	240
	TEELPVVKIGNPKDLKPGEWVAIAGAPFGFDNSVTAGIVSAKGRSLPNESYTPFIQTDVA					
a986	TEELPVVKIGNPKDLKPGEWVAIAGAPFGFDNSVTAGXSAKGRSLPNESYTPFIQTDVA					
	190	200	210	220	230	240

m986.pep	250	260	270	280	290	300
	INPGNSGGPLFNLKGQVVGINSQIYSRSGGFMGISFAIPIDVAMNVAEQLKNTGKVQRGQ					
a986	INPGNSGGPLFNLKGQVVGINSQIYSRSGGFMGISFAIPIDVAMNVAEQLKNTGKVQRGQ					
	250	260	270	280	290	300

m986.pep	310	320	330	340	350	360
	LGVIIQEVSYGLAQSFGLDKAGGALIAKILPGSPAERAGLQAGDIVLSLDGGEIRSSGDL					
a986	LGVIIQEVSYGLAQSFGLDKAGGALIAKILPGSPAERAGLQAGDIVLSLDGGEIRSSGDL					
	310	320	330	340	350	360

m986.pep	370	380	390	400	410	420
	PVMVGAITPGKEVSLGVWRKGEEITIKVKGNAAEHIGASSKTDEAPYTEQQSGTFSVES					
a986	PVMVGAITPGKEVSLGVWRKGEEITIKVKGNAAEHIGASSKTDEAPYTEQQSGTFSVES					
	370	380	390	400	410	420

m986.pep	430	440	450	460	470	480
	AGITLQTHTDSSGGHLVVVRVSDAAERAGLRRGDEILAVGQPVNDEAGFRKAMDKAGKN					
a986	AGITLQTHTDSSGGHLVVVRVSDAAERAGLRRGDEILAVGQPVNDEAGFRKAMDKAGKN					
	430	440	450	460	470	480

m986.pep	490	500				
	VPLLIMRRGNTLFIALNLQX					
a986	VPLLIMRRGNTLFIALNLQX					
	490	500				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2973>:
 g987.seq

1 ATGAAAACAC GCAGCCTCAT TTCCCTTTA TGCCTCCTTC TCTGTTCATG

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51 TTCTTCATGG TTGCCCCAC TGGAAGAACG GACGAAAGC CGTCATTTA
101 ATACTTCAA ACCTGTCTC CTGGACAACA TCCTGAAAT CCGGCACACC
151 CCTCATACCA ACGGGCTATC CGACATCTAC CTGCTGACG ACCCCCACGA
201 AGCCTTGCC GCCCGCGCC CGCTTATCGA ATCTGCCGA CACAGCCTCG
251 ATTTGCAATA CTACATTGG CGAACAGCA TTTCCGGAG GCTGCTGTT
301 AACCTCATGT ACCTGCCG agaacgcggc GTGCGCTAC GCCTGCTGTT
351 ggacgacaAC AACACgcgcg gcttggacg ttcctGCTC GCCCTCGACA
401 GCCATCCCAA TAtctaagtG CGCCTGTTCA ACCCCCTcg CCTACGCAA
451 TGGCGCGCAC TCGGCTACCT GACCGACTTC CCCCGCTCA ACCGCCGAT
501 GCACAACAAA TCCTTACCG CCGACAAACCG CGCCACCAT ATCGGCGGAC
551 GCAATATCGG CGACGAATAC TTCAAAGTCG GTGAGGACAC CGTTTCGCC
601 GACCTGGACA TCCTCGCCAC CGGCAGCGTC GTCGGCGAAG TATCGCACGA
651 CTTCGACCGC TACTGGCAA GCCATTCCGC CCACAAACGCC ACGCGCATCA
701 TCCGCAGCGG CAACATCGC AAGGGTCTTC AAGCACTCGG ATACAACGAC
751 GAAACATCCA GACACGCGCT CTCGCGCTAC CGCGAAACCG TCGAACAGTC
801 GCCCCCTCTAC CAAAAAAATAC AGACGGGACG CATCGACTGG CAGAGCGTCC
851 AAACCCGCGC GATCAGCGAC AGCCCTGCAA AAGGACTCGA CCGCGACCGC
901 CGAAACCCG CGATTGCCGG GAGGCTGCAA GACCGCTCA AACAGCCGAA
951 AAAAAGCGTC TATCTGGTTT CACCTATTG CGTCCCTACA AAATCCGGCA
1001 CAGACGCACT GGCAAAACTG GTGCAGGACG GCATAGACGT TACCGTCTG
1051 ACCAACTCGC TACAGGCGAC CGACGTTGCC GCCGTTCCATT CCGGCTACGT
1101 CAAATACCGA AAACCGCTGC TCAAAGCCGG CATCAAACTC TACGAGCTGC
1151 AACCCAACCA TGCCGCCCCC GCCACAAAAG ACAAAAGGCCT GACCGGCAGC
1201 TCCGTAACCA GCCTGCTATGC CAAAACCTTC ATTGTGGacg gCAAACGCAT
1251 CTTCATGGC TCATTCAACC TCGACCCCCCG TTCCGACCGG CTCAATACCG
1301 AAATGGGCGT CGTCATCGAA AGCCCCAAAAA TCGCAGAACAA GATGGAGCGC
1351 AccctCGCCG AtacCACACC CGAACATCGCC TACCGCGTTA CCCTCGACAA
1401 ACACAAACCGC CTGCAATGGC ACGATCCCGC CACCCGAAAAA ACCTACCCGA
1451 ACGAACCCGA AGCCAAACTT TGGAAACGCA TCGCCGCAAA AATCCTATCC
1501 CTGCTGCCA TCGAAGGTTT ATTATAG

```

This corresponds to the amino acid sequence <SEQ ID 2974; ORF 987.ng>:

g987.pep

```

1 MKTRSLISLL CLLLSCSSW LPPLERTES RHFNTSKPVL LDNIQIRHT
51 PHNNGLSDIY LLDDPFHEAFA ARAALIESAE HSLLDQYYIW RNDISGRLLF
101 NLMYLAAERG VRVRLLLDDN NTRGLDDLL ALDSHPNI*V RLNPVFLRK
151 WRALGYLTDF PRLNRRMHNK SFTADNRATI LGGRNIGDEY FKVGEDTVFA
201 DLDILATGSV VGEVSHDFDR YWASHSAHNA TRIIRSGNIG KGLQALGYND
251 ETSRHALLRY RETVEQSPLY QKIQTGRIDW QSVQTRLISD SPAKGLDRDR
301 RKPPIAGRQLQ DALKQPEKSV YLVSPYFVPT KSGTDALAKL VQDGIDVTVL
351 TNSLQATDVA AVHSGYVKYR KPLLKAGIKL YELQPNHAVP ATKDKGLTGS
401 SVTSLHAKTF IVDGKRIFIG SFNLDPRSAR LNTEMGVVIE SPKIAEQMER
451 TLADTTPEYA YRVTLKDHN R LQWHDPATRK TYPNEPEAKL WKRIAAKILS
501 LPPIEGLL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2975>:

m987.seq

```

1 ATGAAAACAC GCAGCCTAAT TTCCCTTTTA TGCCCTCTTC TCTGTTCATG
51 TTCTTCATGG TTGCCCCAC TGGAAGAACG GACGAAAGC CGTCATTTCA
101 ATACTTCAA ACCCGTCCGC CTGGACAACA TCCTGAAAT CCGGCACACC
151 CCTCATACCA ACGGGCTATC CGATATCTAT CTGTTGACG ACCCCCACGA
201 AGCCTTGCC GCCCGCGCC CGCTTATCGA ATCTGCCGA CACAGCCTCG
251 ATTTGCAATA CTACATCTGG CGAACAGACA TTTCCGGAG GCTGCTGTT
301 AACCTCGTGT ACCTTGCCGC AGAACCGCGT GTGCGCTAC GCCTGCTGTT
351 GGACGACAAC AACACGCGCG GATTGGACGA CCTCTGCTT GCCCTCGACA
401 GCCATCCCAA TATCGAAGTG CGCCTGTTCA ACCCCTCGT CTTACGAAAA
451 TGGCCGCGCAC TCGGCTACCT GACCGACTTC CCCCCGCTCA ACCGCCGAT
501 GCACAACAAA TCCTTACCG CGACAAACCG CGCCACCAT ATCGGCGGAC
551 GCAATATCGG CGACGAATAC TTCAAAGTCG GTGAGGACAC CGTTTCGCC
601 GATTGGACA TCCTCGCCAC CGGCAGCGTC GTCGGCGAAG TATCGCACGA
651 CTTCGACCGC TACTGGCAA GCCATTCCGC CCACAAACGCC ACGCGCATCA
701 TCCGCAGCGG CGACATCGGC AAGGGTCTTC AAGCACTCGG ATACAACGAC
751 GAAACGTCCA GACACCGCGT CCTGCGCTAC CGCGAAACCG TCGAACAGTC
801 GCCCCCTCTAC CAAAAAAATAC AGACAGGATG CATCGACTGG CAGAGCGTCC
851 GAACCCGCGC CATCAGCGAC GACCCCTGCAA AAGGACTCGA CCGCGACCGC

```

```

901 CGCAAACCGC CGATTGCCGG GCGGCTGCAA GACGCGCTCA AACAGCCCGA
951 AAAAAGCGTC TATCTGGTTT CACCCTATT CGTTCCCACA AAATCCGGCA
1001 CAGACGCACT GGCAAAACTG GTGCAGGACG GCATAGACGT TACCGTTCTG
1051 ACCAACTCGC TGCAGGCAGC CGACGTTGCC GCCGTTCCATT CCGGCTATGT
1101 CAAATACCGA AAACCGCTGC TCAAAGCCGG CATCAAACTC TACGAGCTGC
1151 AACCCAACCA TGCGCTCCCC GGCACAAAAG ACAAAAGGCCT GACCGGGCAGC
1201 TCCGTAACCA GCCTGCACGC CAAACACCTTC ATTGTGGACG GCAAACACGAT
1251 CTTCATCGGT TCGTCAACC TCGACCCCCG TTCCGCGCGT CTCAACACCG
1301 AAATGGGGGT TGTTATCGAA AGCCCCAAAAA TCGCAGAACAA GATGGAGCGC
1351 ACCCTTGCCG ATACCACACC CGCCTACGCC TACCGCGTTA CCCTCGACAG
1401 GCACAACCGC CTGCAATGGC ACGATCCCCG CACCCGAAAA ACCTACCCGA
1451 ACGAACCGA AGCCAAACTT TGGAAACGCA TCGCCGCAAA AATCCTATCC
1501 CTGCTGCCA TAGAAGTTT ATTATAG

```

This corresponds to the amino acid sequence <SEQ ID 2976; ORF 987>:

m987.pep

```

1 MKTRSLISLL CLLLCSCSSW LPPIEERTES RHFNTSKPVR LDNIQIRHT
51 PHTNGLSDIY LLNDPHEAFA ARAALIESAE HSLLDQYYIW RNDISGRLLF
101 NLVYLAERG VRVRLLLLDDN NTRGLDDLLL ALDSHPNIEV RLFPNPVLRK
151 WRALGYLTDF PRLNRRMHNK SFTADNRATI LGGRNIGDEY FKVGEDTVFA
201 DLDILATGSV VGEVSHDFDR YWASHSAHNA TRIIRSGDIG KGLQALGYND
251 ETSRHALLRY RETVEQSPLY QKIQTGCIDW QSVRTRLISD DPAKGLDRDR
301 RKPPIAGRRLQ DALKQPEKSV YLVSPYFVPT KSGTDALAKL VQDGIDVTVL
351 TNSLQATDVA AVHSGYVKYR KPLLKAGIKL YELQPNHAVP ATKDKGLTGS
401 SVTSLHAKTF IVDGKRIFIG SFNLDPRSRAR LNTEMGVVIE SPKIAEQMER
451 TLADTTPAYA YRVTLDRHNR LQWHDPATRK TYPNEPEAKL WKRIAAKILS
501 LLPIEGLL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m987/g987 97.8% identity in 508 aa overlap

	10	20	30	40	50	60
m987.pep	MKTRSLISLLCLLLCSCSSWLPPIEERTESRHFNTSKPVRLDNIQIRHTPHTNGLSDIY	: : : : : : : : : :	: : : : : : : : : :	: : : : : : : : : :	: : : : : : : : : :	: : : : : : : : : :
g987	MKTRSLISLLCLLLCSCSSWLPPIEERTESRHFNTSKPVLLDNILQIRHTPHNNGLSDIY	: : : : : : : : : :	: : : : : : : : : :	: : : : : : : : : :	: : : : : : : : : :	: : : : : : : : : :
	10 20 30 40 50 60	10 20 30 40 50 60	10 20 30 40 50 60	10 20 30 40 50 60	10 20 30 40 50 60	10 20 30 40 50 60
	70 80 90 100 110 120	70 80 90 100 110 120	70 80 90 100 110 120	70 80 90 100 110 120	70 80 90 100 110 120	70 80 90 100 110 120
m987.pep	LLNDPHEAFAARAALIESAEHSLLDQYYIWRNDISGRLLFNVLVYLAERGVVRLLLDDN	: : : : : : : : : : :	: : : : : : : : : : :	: : : : : : : : : : :	: : : : : : : : : : :	: : : : : : : : : : :
g987	LLDPHEAFAARAALIESAEHSLLDQYYIWRNDISGRLLFNLMYLAAERGVVRLLLDDN	70 80 90 100 110 120	70 80 90 100 110 120	70 80 90 100 110 120	70 80 90 100 110 120	70 80 90 100 110 120
	130 140 150 160 170 180	130 140 150 160 170 180	130 140 150 160 170 180	130 140 150 160 170 180	130 140 150 160 170 180	130 140 150 160 170 180
m987.pep	NTRGLDDLLLALDSHPNIEVRLFNPFPVLRKWRALGYLTDFPRLNRRMHNKSFADNRATI	: : : : : : : : : : :	: : : : : : : : : : :	: : : : : : : : : : :	: : : : : : : : : : :	: : : : : : : : : : :
g987	NTRGLDDLLLALDSHPNIXVRLFNPFPVLRKWRALGYLTDFPRLNRRMHNKSFADNRATI	130 140 150 160 170 180	130 140 150 160 170 180	130 140 150 160 170 180	130 140 150 160 170 180	130 140 150 160 170 180
	190 200 210 220 230 240	190 200 210 220 230 240	190 200 210 220 230 240	190 200 210 220 230 240	190 200 210 220 230 240	190 200 210 220 230 240
m987.pep	LGGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFDRYWASHSAHNATRIIRSGDIG	: : : : : : : : : : :	: : : : : : : : : : :	: : : : : : : : : : :	: : : : : : : : : : :	: : : : : : : : : : :
g987	LGGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFDRYWASHSAHNATRIIRSGNIG	190 200 210 220 230 240	190 200 210 220 230 240	190 200 210 220 230 240	190 200 210 220 230 240	190 200 210 220 230 240
	250 260 270 280 290 300	250 260 270 280 290 300	250 260 270 280 290 300	250 260 270 280 290 300	250 260 270 280 290 300	250 260 270 280 290 300
m987.pep	KGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGCIDWQSVRTRLISDDPAKGLDRDR	: : : : : : : : : : :	: : : : : : : : : : :	: : : : : : : : : : :	: : : : : : : : : : :	: : : : : : : : : : :
g987	KGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGRIDWQSVPQLRISDSPAKGDRDR	250 260 270 280 290 300	250 260 270 280 290 300	250 260 270 280 290 300	250 260 270 280 290 300	250 260 270 280 290 300
	310 320 330 340 350 360	310 320 330 340 350 360	310 320 330 340 350 360	310 320 330 340 350 360	310 320 330 340 350 360	310 320 330 340 350 360
m987.pep	RKPPIAGRLQDALQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTVLTNSLQATDVA					

g987	RKPPIAGRQLDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTVLTNSQLQATDVA
	310 320 330 340 350 360
m987.pep	AVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTSLHAKTFIVDGKRIFIG
g987	AVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTSLHAKTFIVDGKRIFIG
	370 380 390 400 410 420
m987.pep	SFNLDPRSARLNTEMGVVIIESPKIAEQMERTLADTPAYAYRTLDRHNRQLQWHDPATRK
g987	SFNLDPRSARLNTEMGVVIIESPKIAEQMERTLADTPAYAYRTLDKHNRQLQWHDPATRK
	430 440 450 460 470 480
m987.pep	TYPNEPEAKLWKRIAAKILSLLPIEGLLX
g987	TYPNEPEAKLWKRIAAKILSLLPIEGLLX
	490 500 509

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2977>:

a987.seq
1 ATGAAAACAC GCAGCCTAAT TTCCCTTTA TGCCCTCTTC TCTGTTCATG
51 TTCTTCACTGG TTGCCCCAC TGGAAAGAACG GACGGAAAGC CGTCATTCA
101 ATACTTCAA ACCCGTCCGC CTGGACAACA TCCTGCAAAT CCGGCACACC
151 CCTCATACCA ACGGGCTATC CGATATCTAT CTGTTGAACG ACCCCCCACGA
201 AGCCTTGCC GCCCGCGCC CGCTTATCGA ATCTGCGGAA CACAGCTCG
251 ATTTGCAATA CTACATCTGG CGCAACGACA TTTCGGCCG ACTGCTGTT
301 AACCTCGTGT AACCTTGGCC AGAACCGGGT GTGCGCGTAC GCCTGCTGTT
351 GGACGAAAC AACACGCGC GATGGACGA CCTCTGCTC GCCCCGACACA
401 GCCATCCAA TATCGAAGTG CGCCTGTTCA ACCCTTCTCGT CTTACGAAAA
451 TGGCGCGCAC TCGGCTACCT GACCGACTTC CCCCACCTCA ACCGGCGCAT
501 GCACAAACAAA TCCTTACCG CCGACAACCG CGCCACCCATA CTCGGCGGAC
551 GCAATATCGG CGACGAATAC TTCAAAGTCG GTGAGGACAC CGTTTCGCCC
601 GACCTGGACA TCCTCGCCAC CGGCAGCGTC GTCGCGAAG TATCGCACG
651 CTTCGACCGC TACTGGGCAA GCCATTCCGC CCACAAACGCC ACGCGCATCA
701 TCCGCAAGCGG CAACATCGGC AAGGGTCTTC AAGCACTCGG ATACAACGAC
751 GAAACGTCA GACACGGCGT CCTGCGCTAC CGCGAAACCG TCGAACAGTC
801 GCCCCCTACT CAAAAAAATAC AGACAGGACG CATCGACTGG CAGAGCGTCC
851 AAACCCGCT CATCAGCGAC GACCTGCAA AAGGACTCGA CCGCGACCGC
901 CGCAAACCGC CGATTGGCG GCGGCTGCAA GACCGCGCTCA AACAGCCG
951 AAAAGCGTC TATCTGGTTT CACCCATTG CGTCCCCACA AAATCCGGCA
1001 CAGACGCACT GGCAAAACTG GTGCAGGACG GCATAGACGT TACCGTCTG
1051 ACCAACTCGC TACAGGCGAC CGACGTGCA CGCGTCCATT CCGGCTATG
1101 CAAATACCGA AAACCGCTGC TCAAAGCCGG CATCAAACCTC TACGAGCTGC
1151 AACCCAACCA TGCCGTCCCT GCCACAAAAG ACAAAAGGCCT GACCGGCAGC
1201 TCCGTAACCA GCCTGCATGC CAAAACCTTC ATTGTGGACG GCAAACGCAT
1251 CTTCACTCGGC TCATTCAACC TCGACCCCCG TTCCGCACGG CTCAAACTG
1301 AAATGGCGT TTGTTATCGAA AGCCCCAAAAA TCGCAGAACAA GATGGAGCGC
1351 ACCCTTGGCG ATACCTCACC CGAATACGCC TACCGCGTTA CCCTCGACAG
1401 GCACAACCGC CTGCAATGGC ACGATCCCCG CACCCGAAAA ACCTACCCGA
1451 ACGAACCCGA AGCCAAACTT TGGAACCGCA TCGCCGCAAA AATCCTATCC
1501 CTGCTGCCA TAGAAAGTTT ATTATAG

This corresponds to the amino acid sequence <SEO ID 550: ORF 2978 a>:

```

a987.pep
 1 MKTRSLSILL CLLLCSRSSW LPPLERETES RHFNTSKPVR LDNILOQIRHT
 51 PHTNGLSDIY LLNDPHEAFA ARAALIESAE HSDLQYYIW RNDISGRLLF
101 NLVYLAERG VRVRLLLDN NTRGLDDLL ALDSHPNIEV RLFNPFPVLRK
151 WRALGYLTDF PRLNRRMHNK SFTADNRATI LGGRNIGDEY FKVGEDTFVA
201 DLDILATGSV VGEVSHDFDR YWASHSAHNA TRIIRSGNIG KGLQALGYN
251 ETSRHALLRY RETVEQSPLY QKIQTGRIDW QSVQTRLISD DPAKGLDRDR
301 RKPPPIAGRLO DALKQPEKSV YLVSPYFVPT KSGTDALAKI VODGIDVTVL

```

351 TNSLQATDVA AVHSGYVKYR KPLLKAGIKL YELQPNHAVP ATKDKGLTGS
 401 SVTSLHAKTF IVDGKRIFIG SFNLDPRSRAR LNTEMGVIE SPKIAEQMER
 451 TLADTSPEYA YRVTLDRHNR LQWHDPATRK TYPNEPEAKL WKRIAAKILS
 501 LLPIESLL*

m987/a987 98.8% identity in 508 aa overlap

	10	20	30	40	50	60
m987.pep	MKTRSLISLLCLLLCSCSSWLPPLEERTESRHFNTSKPVRLDNILQIRHTPHTNGLSDIY 					
a987	MKTRSLISLLCLLLCSCSSWLPPLEERTESRHFNTSKPVRLDNILQIRHTPHTNGLSDIY 10 20 30 40 50 60					
	70	80	90	100	110	120
m987.pep	LLNDPHEAFAARAALIESAEHSSDLQYYIWRNDISGRLLFNLVYLAERGVVRLLLDDN 					
a987	LLNDPHEAFAARAALIESAEHSSDLQYYIWRNDISGRLLFNLVYLAERGVVRLLLDDN 70 80 90 100 110 120					
	130	140	150	160	170	180
m987.pep	NTRGLDDLLLALDSHPNIEVRLFNPVLRKWRALGYLTDFPRLNRRMHNKSFADNRATI 					
a987	NTRGLDDLLLALDSHPNIEVRLFNPVLRKWRALGYLTDFPRLNRRMHNKSFADNRATI 130 140 150 160 170 180					
	190	200	210	220	230	240
m987.pep	LGGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHFDRYWASHSAHNATRIIIRSGDIG 					
a987	LGGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHFDRYWASHSAHNATRIIIRSGNIG 190 200 210 220 230 240					
	250	260	270	280	290	300
m987.pep	KGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGCIDWQSVRTRLISDDPAKGLDRDR 					
a987	KGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGRIDWQSQTTRLISDDPAKGLDRDR 250 260 270 280 290 300					
	310	320	330	340	350	360
m987.pep	RKPPPIAGRLQDALKQPEKSVYLSPYFVPTKSGTDALAKLVQDGIDVTVLTNSLQATDVA 					
a987	RKPPPIAGRLQDALKQPEKSVYLSPYFVPTKSGTDALAKLVQDGIDVTVLTNSLQATDVA 310 320 330 340 350 360					
	370	380	390	400	410	420
m987.pep	AVHSGYVKYRKPLLKAGIKLYELQPNHAVPATDKGLTGSSVTSLHAKTFIVDGKRIFIG 					
a987	AVHSGYVKYRKPLLKAGIKLYELQPNHAVPATDKGLTGSSVTSLHAKTFIVDGKRIFIG 370 380 390 400 410 420					
	430	440	450	460	470	480
m987.pep	SFNLDPRSARLNTEMGVVIESPKIAEQMERTLADTTPAYAYRVTLDRHNRLQWHDPATRK 					
a987	SFNLDPRSARLNTEMGVVIESPKIAEQMERTLADTSPEYAYRVTLDRHNRLQWHDPATRK 430 440 450 460 470 480					
	490	500	509			
m987.pep	TYPNEPEAKLWKRIAALKILSLLPIEGLLX 					
a987	TYPNEPEAKLWKRIAALKILSLLPIESLLX 490 500					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2979>:
 g988.seq

1 ATGAATAAAA ATATTAATAC TTTAAATTAA CGGGAAAAAG ACCCGTTTT

51 AAGTCGTGAA AAACAGCGTT ATGAACATCC TTTGCCAGT CGGgaATGGA
 101 TAATCGAATT GTTGAGCGC AAAGGTGTGC CTTAAAAAT CGAACATCGTT
 151 GCACGCGAGC TGTCGATTAC GGAAGacgag tATGTCTTT TTGAACGCCG
 201 TCTGAaggCG atgCGCGGG AcggcTCAAC CGCCgaggcg
 251 CagtTTGCGc gGCgacaag ctgGATTGG TCAAATGccg Cgtcgaggcg
 301 catAAgGAcg gtttcggctt cgcCGTGCCT CTCATGCCGA TGGAACGAAGG
 351 GGATTCGTT TTATACGAAC GCCAgatgcg tggTGTcatG CACggcgaca
 401 ccgttACCGT CCGTCCGTGc ggtatggaa CGAGGGCccg ccgcGAAGgg
 451 acgtttctGG ATATTGTCGA ACGCGCGCAA AGCAAAGTTG TCAGGCCGTTT
 501 CTATATGGAT AGGGCGTGG CGATTTGGA GCGGAAGAC AAGCGTCTGA
 551 ACCAAAGCAT CGTGGTGGAA CCGGACGGCG TGGCGCGTTT CAAACCCGAA
 601 TCCGGTCAGG TTATCGTCGG CAAAATTGAG GTTATCCCG AGCAAAACCG
 651 GCCTGCAGTG GCAAAAATCA TTGAAGTTT GGGCGATTAT GCCGACAGCG
 701 GGATGGAAt cgAAATTGCC GTGCGCAAGC ATCATTGCC GCAccgaTTC
 751 AGTGAagcgt gtGcCAAATC CGcgaAAAAA AtTcccgacc ATGTACGCAA
 801 AAGCGATTG AAAGGCCGCG TCGATTTGTG CGACCTTCCT TTGGTAACGA
 851 TAGACGGCGA AACGGCGCG GATTTCGACG ACGGGTGTT TGCCGAAAAA
 901 GTGCGACGCA ATTACCGCCT GGTCGTGGCG ATTGGCGATG TCAGCCATTA
 951 TGTCCGCCCT GACGATGCGA TTGATGCAGA TGCTCAAGAA CGCAGTACCA
 1001 GCGTGTATTT CCCGCCCGT ATGATTCCGA TGCTGCCGA AAACCTGTCC
 1051 AACGGCATCT GCTCGCTCAA TCCCAGATGTC GAGCGTTTGT GTATGGTGTG
 1101 CGATATGGTC GTTACCTATG CGGGCAATAT CAAAGAATAC CGCTTCTATC
 1151 CCGCCGTGAT GCGCTCTCAT GCCCCGCTGA CCTACAACCA AGTTGGAAA
 1201 TGGCTTCAG ACGGCATCGG GAATCCGCAC AAAGCCAAA TCGACACGCT
 1251 TTACAAGCTG TTAAAAATTGAG TGCAGAAAAA ACGTCTGGCG CGCGGGGCGG
 1301 TGGAGTTTGA AAGCGTCGA ACCCAGATGA TTTTCGACGA CAACGGAAA
 1351 ATCGAAAAAA TTGTCGCCGT CGTCGCCAAC gatGCCACA AGCTGATTGA
 1401 AGAATGTATG CTGGCCCGA ATGTTTGC GCGGGATTTT CTGTTGAAAAA
 1451 ACAAAACATAc GGCTTTGTT CGCAACCATT TGGGCCCCAC GCCGAAAAAA
 1501 CTCGCCACCC TGCGCGAGCA GCTCGGTCTG TTGGGGCTTC AACTTGGCGG
 1551 CGCGACAAAC CGTCGCCGA AAGACTATGC CGCGCTTGCC GAACAATTCA
 1601 AAGGCAGGCC GGATGCCGA TTGCTGCAAG TCATGATGTT GCGCTCCATG
 1651 CAGCAGGCCG TTTACGAACC GCATTGCGAA GGGCATTTCG GTTGGCTTA
 1701 TGAAGCATAC GCCCCATTa CCTCGCCCAT CCGCCGCTAT CCCGACCTGA
 1751 CGTCACCCCG TGCCATCAAA GCCGTATTGA ACCGGAAAAC CTACACGCCA
 1801 AACAAAAGCT GGCAGGCTT GGGCGTGCAT ACTTCGTTT GCGAACGCCG
 1851 TGCCGACGAT GCTGGCCGCG ATGTGGAAAAA CTGGCTGAAA ACTTATTATA
 1901 TGCGCATAA GGTCGGTGAAT ATTGTGAAG GaaaatCtc ccgggggtgtg
 1951 gcaaaTtttg gaATATTGT CACTTGGAC GATATccata tcgacggct
 2001 ggtacaTATC AGCGatttgg gcaAGATTA TTTCaacttc cggcccgAAA
 2051 TCATGGCAAT CGAAGGCCGA CGCAGCGGC TCCGTTCAA TATGGGGGAC
 2101 AGGGTTGCCG TCCGGGTCGC CGGTGCGGAT TTGGATGATG GAAAAATCGA
 2151 CTTTGTCTTA ATTGCCGGAG AAAGCGGCAG GCGGCGGAAG GTCAAATTAT
 2201 CCGCATCTGC CAAACCGGCA GGGGCGGCCG GGAAAGGGAA ATCGAAAAC
 2251 ACCGCCGAGA AAAAACACAGC CCGATGCCGC AAAGTAAGGG GAAGGGCGT
 2301 GCCTGCCGT GCCGAATCGG GGAAAAGGC AAAGAAACCG GTTCCGATTA
 2351 AGGTCAAAAAA ACGGAAAGGC AAATCATAA

This corresponds to the amino acid sequence <SEQ ID 2980; ORF 988.ng>:

g988.pep

1 MNKNIKSLNL REKDPFLSRE KQRYEHPLPS REWIIELLER KGVP SKIESL
 51 ARELSITEDE YVFFERRLKA MARDGQVLIN RRGAVCAADK LDLVKCRVEA
 101 HKDGFGFAVP LMPMDEGDFV LYERQMRGVH HGDVTVRPA GMDRRRRREG
 151 TFLDIVERAQ SKVVGFRYMD RGVAILEPED KRLNQSIVLE PDGVARFKPE
 201 SGQVIVGKIE VYPEQNRPAV AKIIIEVLGDY ADSGMEIEIA VRKHHLPHRF
 251 SEACAKSAKK I PDHVRKSDL KGRV DLCDLP LVTIDGETAR DFDDAVFAEK
 301 VGRNYRLVVA IADVSHYVRP DDAIDADAQE RSTS VYFP RR MIPMLPENLS
 351 NGICSLNPDV ERLCMVCDMV VTYAGNIKEY RFYP AVMRSH ARLTYNQVWK
 401 WLSDGIGNPH KA QIDTLYKL FKILQKKRLA RGA VE FESVE TQMIFDDNGK
 451 IEKIVPVVRN DAHKLIEECM LAANVCAADF LLKNKHTALF RNHLGPTPEK
 501 LATLREQQLGL LGLOLGGDN PSPKDYAALA EQFKGRPDAE LLQVMMLRSM
 551 QOAVYEPHCE GHFGLAYEAY AHFTSPIRYY PDLTVHRAIK AVLN RKTYP
 601 NKS WQALGVH TSFCERRADD AGRD VENWLK TYMMRD KVGE IFEGKISRGV
 651 ANFGIFVTL D IHIDGLVHI S DLGEDYFNF RPEIMAIEGE RSGIRFNMGD
 701 RVAVRVARAD LDDGKIDFVL IAGESGRRRK VKLSASAKPA GAAGKGKSKT
 751 TAEKKTARCG KVRGRGPV AVESGKKAKKP VPIKVKKRKG KS*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2981>:

m988.seq	(partial)
1	..ACAGTTCTGG ATATTGTCGA ACGCGCGCAA AGCAAAGTGG TCGGCCGT
51	CTATATGGAT AGGGGCGTGG CGATTTGGA GCGGAAGAC AAGCGTCTGA
101	ACCAAAGCAT CGTATTGGAA CCGGACGGCG TGGCGCGTTT CAAACCTGAA
151	TCCGGTCAGG TCATCGCG CGAAATTGAG GTTATCCTG AGCAAAACCG
201	GCCGGCAGTG GCAAAATCA TCGAAGTTT GGGCGATTAT GCCGACAGCG
251	GCATGGAGAT TGAAATTGCC GTGCCAAGC ATCATTTGCC GCACCAATT
301	AGTGAAGCGT GTGCCAAGC TCGAAAAAAA ATTCCCGTCC ATGTACGCAA
351	AAGCGATTTG AAAAGGCCGCG TCGATTGCG CGACCTGCCT TTGGTAACGA
401	TAGACGGCGA AACGGCGCG GATTTCGACG ACGGGGTGT TGCCGAAAAA
451	GTCGGACGCA ATTACCGTCT GGTCGTGGCG ATTGCGGATG TCAGCCATTA
501	TGTCCGCCCT GACGATGTGA TTGATGCAGA TGCTCAAGAA CGCAGTACCA
551	GCGTATATT CCCCGCGCGT GTGATTCCGA TGCTGCCGGA AAACCTGTCT
601	AACGGCATTT GCTCGCTCAA TCCCGATGTC GAGCGTTTGT GTATGGTGTG
651	CGATATGGTC GTTACCTATG CGGGCAATAT CAAAGAACAT CGCTTCTACC
701	CCGCCGTAAT GCGCTCTCAT GCCCCGCTGA CCTACAACCA AGTTTGGAAA
751	TGGATTTCAG ACGGCATCGA CCATCCGTAC AAAGCCAAA TCGACACCC
801	TTACAAACTC TTCAAAATCC TTCAGAAAAA GCGTTTCGAA CGCGGCCGCG
851	TGGAGTTTGA AAGCGTCGAA ACCCGAGATGA TTTTCGATGA CAACGGCAA
901	ATCGAAAAAA TCGTCCCCGT TGTCCGCAAC GATGCCACAGA AGCTGATTGA
951	AGAATGTATG CTGGCGCGA ATGTTGCGC AGCGGATTTC CTGTTGAAAA
1001	ACAAGCATAAC GGCCTTGTTC CGCAACCATT TGGGCCAAC GCCCAGAAA
1051	CTCGCCACCC TGCAGGAGCA GCTCGGTCTG TTGGGGCTTC AACTTGGCGG
1101	CGGCGACAAC CCGTCGCCGA AAGACTATGC CGCGCTTGTC GAACAATTCA
1151	AAGGCAGACC TGATGCCGAA TTGCTGCAAG TCATGATGTT GCGCTCCATG
1201	CAGCAGGCAGG TTTACGAACC GCATTGCGAC GGACACTTTG GTCTTGCCTA
1251	CGAAGCATAAC GCCCCACTCA CCTCGCCCAT CGCGCGCTAT CCCGACCTGA
1301	CCGTACACCG CGCCATCAA GCGGTGTTGA ATCAGCAAAC CTACACGCCA
1351	AAAAAAAGCT GGCAGGCTTT GGGCGTGCAT ACCTCGTTCT GTGAGCGCCG
1401	TGCCGACGAC GCCAGCCGCG ACCTGGAAAAA CTGGCTGAAA ACCTATTATA
1451	TGCGCGATAA GGTGGCGAA GTATTGCAAG GTAAAATCTC CGGCATGACC
1501	AGTTTTGGTA TCTTTGTAAC ACTGGACGGC ATCCACATTG ACGGCTTGGT
1551	GCATATCAGC GATTGGCG AAGACTATTT CAACTTCCGC CCCGAAATCA
1601	TGGCAATCGA AGGCGAACGC AGCGGCATCC GTTCAACAT GGGGGACAGG
1651	GTTGCCGTCC GGGTCGCCCG TGCCGATTG GATGACGGAA AAATCGATT
1701	TGTCTGATT GCCGGGGGGG GCGGCAGGGG GCGGAAAGTT AAATCATCCG
1751	CGTCTGCCAA ACCGGCAGGG ACGGCGGGGA AAGGGAAGCC GAAAACCGCC

1400

1801 GCCCGAGAAAA AACAGCCCG AGGGGGCAAA GTAAGGGGAA GGGGCGCGTC
1851 TGCCGCCGCA GAATCGAGGA AAAAGGCAGA GAAACCGGTT CCGATTAAAGG
1901 TAAAAAAACG GAAAGGCAAA TCATAA

This corresponds to the amino acid sequence <SEQ ID 2982; ORF 988>:

m988.pep (partial)

1 . . TVLDIVERAQ SKVVGFRFYMD RGVAILEPED KRLNQSIVLE PDGVARFKPE
51 SGQVIVGEIE VYPEQNRPAV AKIIIEVLGDY ADSGMIEIEIA VRKHHLPHQF
101 SEACAKAAKK IPVHVRKSDL KGRVDLRDL P LVTIDGETAR DFDDAVFAEK
151 VGRNYRLVVA IADVSHYVRP DDVIDADAQE RSTS VYFP RR VIPMLPENLS
201 NGICSLNPDV ERLCMVCDMV VTYAGNIKEY RFYPAVMRSH ARLTYNQVWK
251 WISDGIDH PY KA QIDTLYKL FKILQKKRFE RG AVEFESVE TQMIFDDNGK
301 IEKIVPVVRN DAHKLIEECM LAANVCAADF LLKNKH TALF RNHLGPTPEK
351 LATLREQLGL LGLQLGGDN PSPKD YAA LV EQFKGRPDAE LLOVMMLRS M
401 QQAVYEPHCD GHFGLAYEAY AHFTSPIRRY PD LT VRAIK AVLNQQT YTP
451 KKS WQALGVH TSFCERRADD ASRD VENWLK TY YM RD KVGE V FEGKISGM T
501 SFGIFVTL DG IHIDGLVHS DLGEDYFNFR PEIMAIEGER SGIRFNMGDR
551 VAVRVARADL DDGKIDFVLI AGGSGRGRKV KSSASAKPAG TAGKGPKTA
601 AEKKTARGGK VRGRGASAAA ESRKKAKKPV PI KVKKRKGK S*

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m988/g988 94.2% identity in 642 aa overlap

m988.pep				10	20	30
			TVLDIVERAQSKVVGFRFYMDRGVAILEPED			
g988	LYERQMRGVMHGDVTVRPAGMDRRGRREGTF	L	DIVERAQSKVVGFRFYMDRGVAILEPED			
	130	140	150	160	170	180
	40	50	60	70	80	90
m988.pep	KRLNQSIVLEPDGVARFKPESGQVIVGEIEVY	P	PEQNRPAVAKIIEVLGDYADSGMEIEIA			
g988	KRLNQSIVLEPDGVARFKPESGQVIVGKIEV	Y	YPEQNRPAVAKIIEVLGDYADSGMEIEIA			
	190	200	210	220	230	240
	100	110	120	130	140	150
m988.pep	VRKHHLPHQFSEACAKAAKKIPVHVRKS	D	LKGDRVLDLPLVTIDGETARDFDDAVFAEK			
g988	VRKHHLPHRFSEACAKSAKKIPDHVRKS	D	LKGDRVLDLCDPLVTIDGETARDFDDAVFAEK			
	250	260	270	280	290	300
	160	170	180	190	200	210
m988.pep	VGRNYRLVVAIADVSHYVRPDDVIDADA	Q	ERESTSVYFPRRVIPMLPENLSNGICSLNPDV			
g988	VGRNYRLVVAIADVSHYVRPDDAIDADA	Q	ERESTSVYFPRRMIPMLPENLSNGICSLNPDV			
	310	320	330	340	350	360
	220	230	240	250	260	270
m988.pep	ERLCMVCDMMVTYAGNIKEYRFYPAVMRSH	A	ARLTYNQVWKWISDGDIDHPYKAQIDTLYKL			
g988	ERLCMVCDMMVTYAGNIKEYRFYPAVMRSH	A	ARLTYNQVWKWLSDGGIGNPHKAQIDTLYKL			
	370	380	390	400	410	420
	280	290	300	310	320	330
m988.pep	FKILQKKRFERGAVEFESETQMIFDDNGKIE	K	KIVPVVRNDAHKLIEECMLAANVCAADF			
g988	FKILQKKRFLARGAVEFESVETQMIFDDNGKIE	K	KIVPVVRNDAHKLIEECMLAANVCAADF			
	430	440	450	460	470	480
	340	350	360	370	380	390
m988.pep	LLKNKHTALFRNHLGPTPEKLATLREQLGL	L	LLGGDNPSPKDYAA	LV	EQFKGRPDAE	
g988	LLKNKHTALFRNHLGPTPEKLATLREQLGL	L	LLGGDNPSPKDYAA	LA	EOKGRPDAE	

1401

	490	500	510	520	530	540
m988 . pep	400	410	420	430	440	450
	LLQVMMRLSMQQAVYEPHCDGHFLAYEAYAHFTSPIRYPDLTVHRAIKAVLNRQTYTP					
g988	550	560	570	580	590	600
m988 . pep	460	470	480	490	500	509
	KKSWQALGVHTSFCERRADDASRDVENWLKTYYMRDKVGEVFEKGIS-GMTSFGIFVTLD					
g988	610	620	630	640	650	660
m988 . pep	510	520	530	540	550	560
	GIHIDGLVHISDLGEDYFNFRPEIMAIEGERSGIRFNMGDRVAVRVARADLDDGKIDFVL					
g988	670	680	690	700	710	720
m988 . pep	570	580	590	600	610	620
	IAGGSGRGRKVKSASAKPAGTAGKGPKTAEEKKTARGGKVRGRGASAAAESRKAKKP					
g988	730	740	750	760	770	780
m988 . pep	630	640				
	VPIKVKKRKGKSX					
g988		VPIKVKKRKGKSX				
	790					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2983>:

a988 . seq	1	ATGAATAAAA ATATTAAATC TTTAAATTAA CGGGAAAAAG ACCCGTTTT
	51	AAAGTCGTGAA AAACAGCGTT ATGAACATCC TTTGCCAGT CGGGAATGGA
	101	TAATCGAGCT GCTTGACGT AAAGGCCTAC CATCCAAGAT TGAAGCTTG
	151	GTACCGAAT TGTCGATTAA GGAAGAAAGAG TACGAATTAA TCGAACGTCG
	201	TCTGAAGGCG ATGGCGCGGG ACGGTCAGGT TTTAATCAAC CGTCGGGGCG
	251	CGGTTTGCCTC GCGGGACAAA TTGGATTTCG TCAAATGCCG TGTCAGGCG
	301	CACAAAGACC GCTTCGGTT CGCCGTGCCG CTCACGCCG CCAAAGACGG
	351	TGATTTGTC TTGTACGAAC GCGAGATGCCG CGGCATTATG CACGGCGATA
	401	TTGTCACTGT TCGTCCTGCCG GGCATGGACG GTAGGGCCG CCGCGAAGGG
	451	ACGGTTCTGG ATATTGTCGA ACGCGCGCAA AGCAAAGTGG TCAGGCCGTT
	501	CTANATGGAT AGGGCGTGG CGATTTTGGAA GCCGGAAGAC AACCGTCTGA
	551	ACCAAAGCAT CGTATTGGAA CCGGACGGCG TGGCGCGTT CAAACCTGAA
	601	TCCGGTCAGG TCATCGTCGG CGAAATTGAG GTTTATCCTG AGCAAAACCG
	651	GCCGGCAGTG GCAAAATCA TCGAAGTTTT GGGCATTAT GCGACAGCG
	701	GCATGGAGAT TGAAATTGCCG GTGCGCAAGC ATCATTGCC GCACCAATT
	751	AGTGAAGCGT GTGCCAAAGC CGCGAAAAAA ATTCCCGACC ATGTACGCAA
	801	AAGCGATTG AAAGGGCGCG TCGATTTGCCG CGACCTGCCT TTGTTAACGA
	851	TAGACGGCGA AACGGCTCGA GATTTTGACG ATGCGGTGTT TGCGAGAAA
	901	ATCGGACGCG ATTACCGTCT GGCTGTGGCG ATTGCCGATG TCAGCCATTA
	951	TGTCCGCCCC GATGACGCTA TCGACACGGG CGCTCAGGAA CGCAGCACCA
	1001	GTGTTTACTT CCCGCCCGC GTGATTCCCA TGTGCGCGA AAACCTGTCC
	1051	AACGGCATCT GCTCGCTCAA TCCTCATGTC GAGCGTTTGT GTGTGGTGTG
	1101	CGATATGGTT ATCACTTACG CGGGCAATAT CAAAGAATAC CGCTTCTACC
	1151	CCGCCGTGAT GCGCTCTCAT GCCCGCCTGA CCTACAACCA AGTTGGAAA
	1201	TGGCTTTCAG CGGGCATCGA GCATCCGTT AAAACCCAAA TCGACACGCT
	1251	TTACAAACTC TTCAAAATCC TTCAGAAAAA CGCTTGCAGA CGCGGGCGG
	1301	TGGAGTTGA CAGCATCGAA ACCCAAATGC TTTTCGACGA CAACGGTAAA
	1351	ATTGAAAAAA TCGTCCCCGT TGTCGCAAC GATGCCACA AGCTGATTGA
	1401	AGAATGTATG TTGGCGGCAA ACGTTGCGC AGCGGATTTT CTGTTGAAAA
	1451	ACAAGCATAC CGCATTGTC CGCAACCATT TGGGGCCAC GCGGAAAAAA
	1501	CTCGCCGCCT TGCAGCGAGCA GCTCGGTCTG TTGGGGCTTC AACTTGGCGG
	1551	CGCGACAAAC CCGTCGCCGA AAGACTATGC CGCGCTTGCC GGACAGTTCA

1601 AAGGCAGGCC GGATGCCGAA TTGCTGCAAG TCATGATGTT GCGCTCCATG
 1651 CAACAGGCCG TTTACGAACC GCATTGCGAC GGACACTTG GTCTTGCCTA
 1701 CGAACATAC GCCCACTTC A CCTCGCCCAT CCGCCGCTAT CCCGACCTGA
 1751 CCGTACACCG CGCCATCAA GCCGTGTTGA ATCAGCAAAC CTACACGCCA
 1801 AAAAAAAGCT GGCAGGCTT GGGCGTGCAT ACCTCGTTCT GTGAGCGCCG
 1851 TGCCGACGAC GCCAGCCGCG ACGTGGAAA CTGGCTGAAA ACCTATTATA
 1901 TGCGCATAA GGTGGCGAA GTATTGAAAG GTAAATCTC CGGCATGACC
 1951 AGTTTGTTA ACTTTGTAAC ACTGGACGGC ATCCACATTG ACGGCTTGGT
 2001 GCATATCAGC GATTGGCG AAGACTATT CAACCTCCGC CCCGAAAATCA
 2051 TGGCAATCGA AGGCGAACGC AGCGGCATCC GTTTCAACAT GGGGGACAGG
 2101 GTTGCCTGCC GGGTCGCCCC TGCCGATTG GATGACGGAA AAATCGATT
 2151 TGTCTGATT GCCGGGGGG A GCGCAGGGG GCGGAAAGTT AAATCATCCG
 2201 CGTCTGCCAA ACCGGCAGGG ACGGCGGGG AAGGGAAAGCC GAAAACGCC
 2251 GCGGAGAAAA AAACAGCCCG AGGCGGAAAG GTAAGGGAA GGGGCGCGTC
 2301 TGCCGCGCA GAATCGAGGA AAAAGGAAAG GAAACCGGTT CCGATTAAGG
 2351 TAAAAAAACG GAAAGGCAAA TCATAA

This corresponds to the amino acid sequence <SEQ ID 2984; ORF 988.a>:

a988.pep

1 MNKNIKSLNL REKDPLSRE KORYEHPLPS REWIIELLER KGVP SKIEAL
 51 VREL SIKEEE YEFFERRLKA MARDGQVLIN RRGAVCAADK LDLV KCRVKA
 101 HKDR FGF AWP LTPAKDGD FV LYER QMRGIM HG DIVTVRPA GM DGR GR REG
 151 TVLD IVERAQ SKV VGR FXMD RGVAILE PED KRLN QSIV LE PDG VAF RKPE
 201 SG OVIV GEIE VYPE QNR PAV AKI IEV LGDY AD SGME IEIA VR KHHL PHQF
 251 SE AC AAKK IP DHVR KSDL KGRV DL RDLP LVT IDGET AR DFDDA VFAEK
 301 I GR NY RL VVA I ADV SHY VRP DDA IDT DAQ E RST SVY FP RR VIP M PL PEN LS
 351 NG IC SLN PHV ERL CVV CDMV ITYAG NI KEY RF YPA VM RSH AR LT YN QV WK
 401 WLSGGIEHPF KT QID TLYKL FK ILQ KKR F RGA VE FDS IE T QML FDD N GK
 451 IE KIV PV VVN DAH KLI EECM LAAN VCA ADL LL KKN HT ALF RN HLG PT PEK
 501 LA AL RE QL GL LGL QL GG DN PSP K DY A ALA G QFK GRP DAE LL QV MM LR SM
 551 QQ AVY EPH CD GH FG LAYE AY AH FT SP IR Y PDL TV HRA IK AV LN Q QT Y TP
 601 KK SW QAL GVH TS FCERR ADD AS RD VEN WLK TY YM RD KV GE VF EG KIS G M T
 651 SFG IF VT LDG IH ID GL VH IS DL GED Y FN FR PEIMA IE GER SG IR FN MG DR
 701 VAV RV VAR ADL DD GKI DF VL AGG SGR GR KV KSSA SAK PAG TAG KG KPK TA
 751 AE KK TARG GK VR RGAS AAA ESR KKAKK PV PI KV KK RKG K S*

m988/a988 97.0% identity in 641 aa overlap

		10	20	30			
m988.pep		TVLD IVERAQ SKV VGR F YMD RG VAI LE PED					
a988	LYER QMRG IM HG DIVTVR PA GMD GR GR REG TV LD IVERAQ SKV VGR F XMD RG VAI LE PED	130	140	150	160	170	180
m988.pep	KRLN QSIV LE PDG VAF RK PES GQV IV GEIE VY PE QNR PAV AKI IEV LGDY AD SGME IEIA	40	50	60	70	80	90
a988	KRLN QSIV LE PDG VAF RK PES GQV IV GEIE VY PE QNR PAV AKI IEV LGDY AD SGME IEIA	190	200	210	220	230	240
m988.pep	VR KHHL PHQ F SE AC AAKK I PV HVR KSDL KGRV DL RDLP LVT IDGET AR DFDDA VFAEK	100	110	120	130	140	150
a988	VR KHHL PHQ F SE AC AAKK I PD HVR KSDL KGRV DL RDLP LVT IDGET AR DFDDA VFAEK	250	260	270	280	290	300
m988.pep	VGR NY RL VVA I ADV SHY VRP D D A QER STS VY F PRR V I PML P EN LS NG IC SLN PD V	160	170	180	190	200	210
a988	I GR NY RL VVA I ADV SHY VRP D D A QER STS VY F PRR V I PML P EN LS NG IC SLN PH V	310	320	330	340	350	360
m988.pep	ERLCMVCDMV VTYAG NI KEY RF YPA VM RSH AR LT YN QV WK W IS DG ID HP YKA QID TLYKL	220	230	240	250	260	270
a988	ERLCVVCDMV VTYAG NI KEY RF YPA VM RSH AR LT YN QV WK W LSGGIEHPF KT QID TLYKL						

1403

	370	380	390	400	410	420
m988.pep	280	290	300	310	320	330
	FKILQKKRFERGAVEFESVETQMIFDDNGKIEKIVPVVRNDAHKLIEECMLAANVCAADF					
a988	430	440	450	460	470	480
	340	350	360	370	380	390
m988.pep	LLKNKHTALFRNHLGPTPEKLATLREQLGLLQLQLGDDNPSPKDYAALVEQFKGRPDAE					
a988	490	500	510	520	530	540
	400	410	420	430	440	450
m988.pep	LLQVMMRLSMQQAVYEPHCDGHFGLAYEAYAHFTSPIRRYPDLTVHRAIKAVLNQQTYTP					
a988	550	560	570	580	590	600
	460	470	480	490	500	510
m988.pep	KKSWQALGVHTSFCCERRADDASRDVENWLKTYYMRDKVGEVFEKGKISGMTSFGIFVTLDG					
a988	610	620	630	640	650	660
	520	530	540	550	560	570
m988.pep	IHIDGLVHISDLGEDYFNFRPEIMAIEGERSGIRFMGDRVAVRVARADLDDGKIDFVLI					
a988	670	680	690	700	710	720
	580	590	600	610	620	630
m988.pep	AGGSGRGRKVKSASAKPAGTAGKGKPATAEKKTARGKVRGRGASAAAESRKKAACKPV					
a988	730	740	750	760	770	780
	640					
m988.pep	PIKVKKRKGKSX					
a988	PIKVKKRKGKSX					
	790					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2985>:

g989.seq

1	ATGACCCCTT	TCACACTGAA	AAAAACCGTC	CTGCTGCTCG	GCACTGCCTT
51	TGCCGGCGCA	TCTGTCCACG	CATCCGGCTA	CCACTTCGGC	ACACAGTCGG
101	TCAACCGCGCA	AAGCACGGCA	AATGCCGCCG	ACGCGTCGAC	CATCTTCTAC
151	ATATCCCGCG	GCCTGACCAA	ACTCGACAGC	AGCCAGATT	CCGTCAACGC
201	CAACATCGTG	CTGCCAGCA	TTCATTTGA	AGCAGATTCC	GCCACCGACT
251	TTACCGGGCT	TCCCCTCCA	GGTTCTAAA	ACGGCAAAAT	CACCAAAACC
301	ACGGTCGAC	CCCACATT	CGCGCATAAC	AAAGTCAACG	ACAATCTGAC
351	CGTGGGCTTG	GGCGTGTACG	TCCCCTCGG	CTCTGCACC	GAATACGAAA
401	AAGATTCG	GTTGCCAAC	AAACATCAACA	AACTCGGTCT	GACCAGCATC
451	GCCGTCGAAC	CTGTCGCCGC	GTGGAAACTC	AACGAACGCC	ATTCCTTCGG
501	CGCAGGCATC	ATCGCCAAAC	ATAATTCCGC	CGAACTGCGC	AAATATGCCG
551	ACTGAGGAAT	CCCAAAAAAA	GCGCAAATGC	TGCAAGCAAC	ACCTTCTAAT
601	CCTACTGCCG	CTGCTCAAAT	CAAGGCCGAC	GGACAGGCCG	ATGTCAAAGG
651	CAGCGATTGG	GGCGTCGGCT	ACCAACTGGC	GTGGATGTGG	GACATCAACG
701	ACCGCGCGCG	C GTGGCGTG	AACTACCGTT	CCAAAGTTTC	ACACACGCTC
751	AAAGGCATG	CCGAATGGGC	GGCAGACGGC	GGCGCGCGA	AACAAACAGTG
801	GAATGACAAT	ATGCTCACAC	CGCTCGGTTA	CACGGCGAAT	AAAAAGCCA
851	GTGTCAAAAT	CGTAAACGCCT	GAGTCTTGT	CCGTACACGG	CATGTACAAA

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901 GTGTCCGACA AAGCCGACCT GTTCGGCAGC GTAACCTGGGA CGCGGCCACAG
951 CCGCTTCAAT AAGGCGGAAC TGTTTTTGAA AAAAGAAAAA AATATTGCTA
1001 ATGGCAAAAAA ATCCGACCGC ACCACCATCA CCCCCAACGT GCGCAACACC
1051 TACAAAGTCG GCTTGGCGG TTCTTATCAA ATCAGCGAAC CGCTGCAACT
1101 GCGCGTCGGC ATCGCTTTG ACAAACCGCC TGTCGGCAAC GCCGACTacc
1151 GCATGAACAG CCTGGCCGAC GGCAACCGCA TCTGTTCTC CGCCGGCATG
1201 AAATACCATCA TCGGCAAAAA CCACGTCGTC GATGCCGCCT ACACCCACAT
1251 CCACATCAAC GACACCGAGC ACCGCACGCG GAAGGCAAGC GGCAACGATG
1301 TGGACAGCAA AGGTGCGTCT TGCGCACGTT TCAAAAACCA CGCCGACATC
1351 ATCGGCCTGC AATACACCTA CAAATTCAAA TAA

```

This corresponds to the amino acid sequence <SEQ ID 2986; ORF 989.ng>:

g989.pep

```

1 MTPFTLKKTV LLLGTAFAAA SVHASGYHFG TQSVNAQSTA NAADASTIFY
51 NPAGLTKLDS SQISVNANIV LPSIHYEADS ATDFTGLPVQ GSKNGKITKT
101 TVAPHIYGAY KVNDNLTVGL GVYVPGFSAT EYEKDSVLRH NINKLGLTSI
151 AVEPVAAWKL NERHSFGAGI IAQHNSAELR KYAD*GIPKK AQMLQATPSN
201 PTAAAQIKAD GHADVKGSWD GVGYQLAWMW DINDRARVGV NYRSKVSHTL
251 KGDAEWAADG AAAKQQWNNDN MLTPLGYTAN EKASVKIVTP ESLSVHGMYK
301 VSDKADLFGD VTWTRHSRFN KAELEFFEKEK NIANGKKSDR TTITPNWRNT
351 YKVGLGGSYQ ISEPLQLRVG IAFDKPPVRN ADYRMNSLPD GNRIWFSAGM
401 KYHIGKNHVV DAAYTHIIHIN DTSYRTAKAS GNDVDSKGAS CARFKNHADI
451 IGLQYTYKFK *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2987>:

m989.seq

```

1 ATGACCCCTT CCGCACTGAA AAAAACCGTC CTGCTGCTCG GCACTGCCCT
51 TGCCGCCGCA TCCGTCCACG CATCCGGCTA CCACTTCGGC ACACAGTCGG
101 TCAACGCCA AAGCACGGCA ATGCCGCCG CCGCAGAACG CGCCGACGCCA
151 TCGACCACCT TCTACAACCC TGCCGGCCTG ACCAAACTCG ACAGCAGCCA
201 GATTCGCCCT AACGCCAACA TCGTGCTGCC CAGCATTCTAT TATGAGGCCG
251 ATTCCGCCAC CGACTTTTACG GGGCTTCCC TCCAAGGTTG GAAAAGCGGC
301 AAAATCACCA AAACCACCGGT CGCGCCCCAC ATCTACGGCG CATACAAAGT
351 CAACGACAAT CTGACCGTGG GCTTGGCGGT GTACGCTCCC TTCCGGCTCTG
401 CCACCGAATA CGAAAAGAGT TCCGTGTTGC GCCACAAACAT CAACAAACTC
451 GGTCTGACCA GCATCGCCGT CGAACCTCTG CCGCCTGGAA AACTCAACGA
501 CCGCCATTCC TTCCGGCGAG GCATCATCGC CCAACATACT TCCGCCGAAC
551 TGCGCAAATA TGCCGACTGG GGGATTAAGA GTAAAGCAGA GATATTGACG
601 GCAAAACCGC CCAAACCTAA CGGTGTAGCC GAAGCTGCAA AAATTCAAGGC
651 CGACGGACAC GCCGATGTCA AAGGCAGCGA TTGGGGCTTC GGCTACCAAC
701 TGGCGTGGAT GTGGGACATC AACGACCGTG CGCGCGTGGG CGTGAACCTAC
751 CGTTCCAAAG TCTCCACAC GCTCAAAGGC GATGCCGAAT GGGCGGCAGA
801 CGGCGCGGGCG GCGAAAGCAA TGTGGAGTAC GATGCTTGCA GCAAACGGCT
851 ACACGGCGAA TGAAAAGCC CGCGTTAAAAA TCCTTACGCC TGAGTCTTTG
901 TCCGTACACG GTATGTACAA AGTGTCCGAT AAAGCCGACC TTTCGGCGA
951 CGTAACTTGG ACGGCCACCA GCGCTTCGA TAAGGCGGAA CTGGTTTTTG
1001 AAAAGAAAAA AACCGTCGTC AAAGGCAAAAT CCGACCGCAC CACCATCACC
1051 CCCAACTGGC GCAACACCTA CAAAGTCGGC TTCCGGGGTT CTTATCAAAT
1101 CAGCGAACCG CTGCAACTGC GCGCCGGCAT CGCTTTGAC AAATCGCCCG
1151 TCCGCAACGC CGACTACCGC ATGAACAGCC TACCCGACGG CAACCGCATC
1201 TGGTTCTCCG CGGGTATGAA ATACCATATC GGTAAAAAAC ACGTCGTGCA
1251 TGCCGCCTAC ACCCACATCC ACATCAACGA CACCAGCTAC CGCACGGCGA
1301 AGGCAAGCGG CAACGGATGTG GACAGCAAAG GCGCGTCTTC CGCACGTTTC
1351 AAAAACACCG CCGACATCAT CGGTCTGCAA TACACCTACA AATTCAAATA
1401 A

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This corresponds to the amino acid sequence <SEQ ID 2988; ORF 989>:

m989.pep

```

1 MTPSALKKTV LLLGTAFAAA SVHASGYHFG TQSVNAQSTA NAAAAEAADA
51 STIFYNPAGL TKLDSSQISV NANIVLPSIH YEADSATDFT GLPVQGSKSG
101 KITKTTVAPH IYGAYKVNDN LTVGTVYV FGSATEYEKD SVLRHNINKL
151 GLTSIAVEPV AAWKLNDRHS FGAGIIAQHT SAEILRKYADW GIKSKAEILT
201 AKPPKPNGVA EAAKIQADGH ADVKGSDWF GYQLAWMWDI NDRAVGVNY
251 RSKVSHTLKG DAEWAADGAA AKAMWSTMLA ANGYTANWEKA RVKIVTPESL
301 SVHGMYKVSD KADLFGDVTW TRHSRFDKAE LVFEKEKTVV KGKSDRTTIT

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351 PNWRNTYKVG FGGSYQISEP LQLRAGIAFD KSPVRNADYR MNSLPDGNI
 401 WFSAGMKYHI GKNHVVDAAY THIHINDTSY RTAKASGNDV DSKGASSARF
 451 KNHADIIGLQ YTYKFK*

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

g989/m989 90.0% identity in 468 aa overlap

g989.pep	10	20	30	40	50		
	MTPFTLKKTVLLGTAFAAASVHASGYHFGTQSVNAQSTANAA-----			DASTIFYNPAGL			
m989	10	20	30	40	50	60	
	MTPSALKKTVLLGTAFAAASVHASGYHFGTQSVNAQSTANAAAEEAADASTIFYNPAGL						
g989.pep	60	70	80	90	100	110	
	TKLDSSQISVNANIVLPSIHYEADSATDFTGLPVQGSKNGKITKTTVAPHIYGAYKVNDN						
m989	70	80	90	100	110	120	
	TKLDSSQISVNANIVLPSIHYEADSATDFTGLPVQGSKSGKITKTTVAPHIYGAYKVNDN						
g989.pep	120	130	140	150	160	170	
	LTVGLGVYVPFGSATEYEKDSDLRHNINKLGLTSIAVEPVAWKLNERHSFGAGIIAQHN						
m989	130	140	150	160	170	180	
	LTVGLGVYVPFGSATEYEKDSDLRHNINKLGLTSIAVEPVAWKLNDRHSGAGIIAQHT						
g989.pep	180	190	200	210	220	230	
	SAELRKYADXGIPKKAQMLQATPSNPTA---AAQIKADGHADVKGSDWGVGYQLAWMWDI						
m989	190	200	210	220	230	240	
	SAELRKYADWGKSKAEILTAKPPKPNGVAEAAKIQADGHADVKGSDWGFQGYQLAWMWDI						
g989.pep	240	250	260	270	280	290	
	NDRARVGVNRSKVSHTLKGDAEWAADGAAAKQQWNDNMLTPLGYTANEKASVKIVTPES						
m989	250	260	270	280	290		
	NDRARVGVNRSKVSHTLKGDAEWAADGAAAKAMWS-TMLAANGYTANEKARVKIVTPES						
g989.pep	300	310	320	330	340	350	
	LSVHGMKYVSDKADLFGDVTWTRHSRFNKAELFFEKEKNIANGKKSDRTTITPNWRNTYK						
m989	300	310	320	330	340	350	
	LSVHGMKYVSDKADLFGDVTWTRHSRFDKAELVFEKEKTVVKKGK-SDRTTITPNWRNTYK						
g989.pep	360	370	380	390	400	410	
	VGLGGSYQISEPLQLRVGIAFDKPPVRNADYRMNSLPDGNIWFSAGMKYHIGKNHVVDA						
m989	360	370	380	390	400	410	
	VGFGGSYQISEPLQLRAGIAFDKSPVRNADYRMNSLPDGNIWFSAGMKYHIGKNHVVDA						
g989.pep	420	430	440	450	460		
	AYTHIHINDTSYRTAKASGNDVDSDKASCARFKNHADIIGLQTYTYKFKX						
m989	420	430	440	450	460		
	AYTHIHINDTSYRTAKASGNDVDSDKASSARFKNHADIIGLQTYTYKFKX						

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2989>:

a989.seq

1	ATGACCCCTT CCGCACTGAA AAAAACCGTC CTACTGCTCG GCAC TGCC TT
51	TGCCGCCGCA TCCGACAAG CCTCCGGCTA CCACTTCGGC ACACAGTCGG
101	TCAACGCGCA AAGCACGGCA AATGCCGCG CCAGCAGAAC CGCCGACGCA
151	TCGACCATCT TCTACAACCC TGCCGGCCTG ACCAAACTCG ACAGCAGCCA
201	GATTTCGGTC AACGCCAACA TCGTGCTGCC CAGCATT CAT TATGAGGC GG
251	ATTCCGCCAC CGACTTTACC GGGCTTCCCG TCCAAGGTTC GAAAAGCGGC

301 AAAATCACCA AAACCACGGT CGCGCCCCAC ATCTACGGCG CATACAAAGT
 351 CAACGACAAT CTGACCGTAG GCTTGGGCCT GTACGTCCCC TTGGTTCTG
 401 CCACCGAATA CGAAAAAGAT TCCGTGTTGC GCCACAACAT CAACAAACTC
 451 GGTCTGACCA GCATGCCGT CGAACCTGTC GCGCGTGGAA AACTAACGA
 501 ACGCCATCC TTCGGCGCAG GCATCATCGC CCAACATACT TCCGCCGAGC
 551 TGCGCAAATA TGCGCACTGG GGGATTATGG AAAAAGCGAA AGCACTAAA
 601 GAAACACCCC CCAATCCAAC TAAAGCCGCC CAAATCAAAG CCGACGGACA
 651 CGCCGATGTC AAAGGCAGCG ATTGGGGCTT CGGCTACCAA CTGGCGTGGA
 701 TGTGGGACAT CAAACGACCGT GCGCGCTGG GCGTAACTA CCGTTCCAAA
 751 GTCTCACACA CGCTCAAAGG CGATGCCGAA TGGGCGGCAG ACGACGCAAT
 801 GGC GAAACAG TTATGGGATG CAAACAAACT CGCACTGCTC GGCTACACGC
 851 CAAGCGAAAA AGCCCGCGT AAAATCGTTA CGCCCGAGTC TTTGTCGCGTA
 901 CACGGTATGT ACAAAAGTGT CGACAAAGCC GACCTGTTG GCGACGTAAC
 951 TTGGACGCGC CACAGCCGCT TCGATAAGGC GGAACCTGGTT TTGAAAAAG
 1001 AAAAAACCAT CGTCAACCGC AAATCCGACC GCACCACCAT CACCCCCAAC
 1051 TGGCGCAACA CCTACAAAGT CGGCTTCGGC GGTTCTTATC AAATCAGCGA
 1101 ACCGCTGCAA CTGCGCGCC GCATCGCTT TGACAAATCG CCCGTCCGCA
 1151 ACGCCGACTA CCGCATGAAC AGCCTGCCCG AGCGCAACCG CATCTGGTTC
 1201 TCCGCCGCGA TGAATACCA TATCGGCAA AACACACGTC TCGATGCCGC
 1251 CTACACCCAC ATCCACATCA ACGACACCAAG CTACCCGACG GCGAAGGGCAA
 1301 GCGGCAACGA TGTGGACAGC AAAGGCAGCGT CTTCCGCACG TTTCAAAAAC
 1351 CACGCCGACA TCATCGGCCT GCAATACACC TACAAATTCA AATAA

This corresponds to the amino acid sequence <SEQ ID 2990; ORF 989.a>:

a989.pep

```

1 MTPSALKKTV LLLGTAFAAA SAQASGYHFG TQSVNAQSTA NAAAAEAADA
51 STIFYNPAGL TKLDSSQISV NANIVLPSIH YEADSATDFT GLPVQGSKSG
101 KITKTTVAPH IYGAYKVNDN LTVGLGVYVP FGSATEYEKD SVLRHNINKL
151 GLTSIAVEPV AAWKLNERHS FGAGIIAQHT SAEILRKYADW GIMEKAKALK
201 ETPPNPTKAA QIKADGHADV KGSDWGFYQ LAWMWDINDR ARVGVNRYRSK
251 VSHTLKGDAE WAADDAMAKQ LWADANKLALL GYTPSEKARV KIVTPESLSV
301 HGMYKVSDKA DLFGDVTWTR HSRFDKAELV FEKEKТИVNG KSDRTTITPN
351 WRNTYKVGF GSYQISEPLQ LRAGIAFDKS PVRNADYRMN SLPDGNIWFE
401 SAGMKYHIGK NHVVDAAYTH IHINDTSYRT AKASGNDVDS KGASSARFKN
451 HADIIGLQYT YKFK*

```

m989/a989

93.1% identity in 467 aa overlap

m989.pep

```

          10      20      30      40      50      60
MTPSALKKTVLLLGTAFAAASVHASGYHFGTQSVNAQSTANAAAAAADASTIFYNPAGL
|||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|

```

a989

```

          10      20      30      40      50      60
MTPSALKKTVLLLGTAFAAASQAQASGYHFGTQSVNAQSTANAAAAAADASTIFYNPAGL
|||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|

```

m989.pep

```

          70      80      90      100     110     120
TKLDSSQISVNANIVLPSIHYEADSATDFTGLPVQGSKSGKITKTTVAPHIYGAYKVNDN
|||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|

```

a989

```

          70      80      90      100     110     120
TKLDSSQISVNANIVLPSIHYEADSATDFTGLPVQGSKSGKITKTTVAPHIYGAYKVNDN
|||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|

```

m989.pep

```

          130     140     150     160     170     180
LTGVLGVYVPFGSATEYEKDSVLRHNINKLGLTSIAVEPVAAWKLDRHSGFAGIIAQHT
|||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|

```

a989

```

          130     140     150     160     170     180
LTGVLGVYVPFGSATEYEKDSVLRHNINKLGLTSIAVEPVAAWKLNERHSGFAGIIAQHT
|||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|

```

m989.pep

```

          190     200     210     220     230     240
SAELRKYADWGIKSKAEILTAKPPKPNGVAEEAKIQADGHADVKGSDWGFYQLAWMWDI
|||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|

```

a989

```

          190     200     210     220     230
SAELRKYADWGIMEKAKALKETPPNPT---KAAQIKADGHADVKGSDWGFYQLAWMWDI
|||||||:|||||:|||||:|||||:|||||:|

```

m989.pep

```

          250     260     270     280     290     299
NDRARVGVNYRSKVSHTLKGDAEWAADGAAKAMW-STMIAANGYTANEKARVKIVTPES
|||||||:|||||:|||||:|||||:|||||:|||||:|

```

a989

```

          250     260     270     280     290     299
NDRARVGVNYRSKVSHTLKGDAEWAADAMAKQLWDANKLALLGYTPSEKARVKIVTPES
|||||||:|||||:|||||:|||||:|||||:|

```

1407

	240	250	260	270	280	290	
m989.pep	300	310	320	330	340	350	359
	LSVHGMVKVSDKADLFGDVTWTRHSRFDKAELVFEKEKTVVKGKSDRTTITPNWRNTYKV						
a989							
	LSVHGMVKVSDKADLFGDVTWTRHSRFDKAELVFEKEKTVVNGKSDRTTITPNWRNTYKV						
	300	310	320	330	340	350	359
m989.pep	360	370	380	390	400	410	419
	GFGGSYQISEPLQLRAGIAFDKSPVRNADYRMNSLPDGNRIWFSAGMKYHIGKNHVVDAA						
a989							
	GFGGSYQISEPLQLRAGIAFDKSPVRNADYRMNSLPDGNRIWFSAGMKYHIGKNHVVDAA						
	360	370	380	390	400	410	419
m989.pep	420	430	440	450	460		
	YTHIHINDTSYRTAKASGNDVDSKGASSARFKNHADIIGLQTYKFKX						
a989							
	YTHIHINDTSYRTAKASGNDVDSKGASSARFKNHADIIGLQTYKFKX						
	420	430	440	450	460		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2991>:

m990.seq	1	ATGTTCAGAG CTCAGCTTGG TTCAAATACT CGTTCTACCA AAATCGGCAG
	51	CGATGCCGAT TTTTCATTTC CAGACAAGCC GAAACCCGGC ACTTCCCATT
	101	ATTTTCCAG CGGTAACACC GATCAAATT CATCGAATA TGGGTATGAC
	151	GAAATCAATA TCCAAGGTA AAATTACAAT AGCGGCATCC TCGCCGTCGA
	201	TAATATGCC GTTGTCAAAA AATATATTAC AGAGAAGTAT GGGGCTGATT
	251	TAAAGCAGGC GGTAAAAAGT CAATTACAGG ATTTATACAA AACAAAGACCG
	301	GAAGCTTGGG CAGAAAATAA AAAACGGACT GAGGGCGT ATATAGCACA
	351	GTTTGAACA AAATTAGTA CGCTCAAACA GACGATGCC GATTTAATT
	401	ATAAAATTGGT AGAAGATTCC GTACTCACT CTCATAGTAA TACATCACAG
	451	ACTAGTCTCA ACAACATCTT CAATAAAAAA TTACACGTCA AAATCGAAAA
	501	CAAATCCCAC GTCGCCGGAC AGGTGTTGGA ACTGACCAAG ATGACGCTGA
	551	AAGATTCCCT TTGGGAACCG CGCCGCCATT CCGACATCCA TACGCTGGAA
	601	ACTTCCGATA ATGCCCGCAT CGCCCTGAAC ACGAAAGATG AAAAAACTGAC
	651	CGTCCATAAG GATTATGCC GCGGCGCGGA TTTCCTGTT GGCTACGAGC
	701	TGCGGGAGTC GGACGAACCC GCCCTGACCT TTGAAGACAA AGTCAGCGGA
	751	CAATCCGGCG TGGTTTGGA ACGCCGGCCG GAAAATCTGA AAACGCTCGA
	801	CGGGCGCAA CTGATTGCGG CAAAAAACGGC GGATTCGGT TCGTTTGCGT
	851	TTAAACAAAA TTACCGGCAG GGACTGTACG AATTATTGCT CAAGCAATGC
	901	GAAGGCGGAT TTTGCTTGGG CGTGCAGCGT TTGGCTATCC CCGAGGCGGA
	951	AGCGGTTTA TATGCCCAAC AGGCTTATGC GGCAAATACT TTGTTTGGGC
	1001	TGCGTCCCGC CGACAGGGGC GACGACGTGT ATGCCGCCGA TCCGTCGGT
	1051	CAAAAATTGT GGCTCGCCTT CATCGCGCAGC CGGTGGCATC AAAATATACG
	1101	GGGCGGGCGC GCTCGCGACG GGTGGCGCAA AGGCGTGCAA ATCGGCGGCC
	1151	AGGTGTTTGT ACGGAAAAT GAAGGCAGCC GACTGGCAAT CGGCGTGATG
	1201	GGCGGGCAGGG CCGGCCAGCA CGCATCAGTC AACGGCAAAG GCGGTGCGGC
	1251	AGGCAGTGAT TTGTATGGTT ATGGCGGGGG TGTTTATGCT GCGTGGCATC
	1301	AGTTGCGCGA TAAACAAACG GGTGCAGTATT TGGACGGCTG GTTGAATAC
	1351	CAACGTTTCA AACACCGCAT CAATGATGAA AACCGTGCAG AACGCTACAA
	1401	AACCAAAGGT TGGACGGCTT CTGTCGAAGG CGGCTACAAAC GCGCTTGTGG
	1451	CGGAAGGCAT TGTGGAAAAA GGCAATAATG TGCGGTTTA CCTACAAACCG
	1501	CAGGCGCAGT TTACCTACTT GGGCGTAAAC GGCAGCTTTA CCGACAGCGA
	1551	GGGGACGGCG GTCGGACTGC TCAGCAGCGG TCAGTGGCAA AGCCGCGCCG
	1601	GCATTGGGGC AAAAACCCGT TTTGCTTGC GTAACGGTGT CAATCTTCAG
	1651	CCTTTGGCG CTTTAATGT TTTGACAGG TCAAATCTT TCGGCGTGGAA
	1701	AATGGACGGC GAAAAACAGA CGCTGGCAGG CAGGACGGCA CTCGAAGGGC
	1751	GGTTCGGTAT TGAAGCCGGT TGGAAAGGCC ATATGTCGGC ACGCATCGGA
	1801	TATGGCAAAA GGACGGACGG CGACAAAGAA GCGCATTGT CGCTCAAATG
	1851	GCTGTTTGA

This corresponds to the amino acid sequence <SEQ ID 2992; ORF 990>:

m990.pep

```

1 MFRAQLGSNT RSTKIGDDAD FSFSDKPKPG TSHYFSSGKT DQNSSEYGYD
51 EINIQGKNYN SGILAVDNMP VVKKYITEKY GADLKQAVKS QLQDLYKTRP
101 EAWAENKKRT EEAYIAQFGT KFSTLKQTMP DLINKLVEDS VLTPHSNTSQ
151 TSLNNIFNKK LHVKIENKSH VAGQVLELTK MTLKDSLWEP RRHSDIHTLE
201 TSDNARIRLN TKDEKLTVHK DYAGGADEF LF GYDVRESDEP ALTFEDKVSG
251 QSGVVLERRP ENLKTLGDRK LIAAKTADSG SFAFKQNYRQ GLYELLLKQC
301 EGGFCLGVQR LAIPEAEAVL YAQQAYAAANT LFGLRAADRG DDVYAADPSR
351 QKLWLRFIGG RSHQNIRGGA AADGWRKGVQ IGGEVFVRQN EGSRLAIGVM
401 GGRAGQHASV NGKGGAAAGSD LYGYGGGVYA AWHLQRDKQT GAYLDGWLQY
451 QRFKHRINDE NRAERYKTKG WTASVEGGYNA ALVAEGIVGK GNNVRFYLQP
501 QAQFTYLGVN GGFTDSEGT A VGLLGSGQWQ SRAGIRAKTR FALRNGVNLIQ
551 PFAAFNVLHR SKSFGVEMDG EKOTLAGRTA LEGRFGIEAG WKGHMSARIQ
601 YGKRTDGDKE AALS LKWL F*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2993>:

a990.seq

```

1 ATGTTTCAGAG CTCAGCTTGG TTCAAATACT CGTTCTACCA AAATCGGCGA
51 CGATGCCGAT TTTTCATTTC CAGACAAGCC GAAACCCGGC ACTTCCCATT
101 ATTTTCCAG CGGTAAAACC GATCAAAATT CATCCGAATA TGGGTATGAC
151 GAAATCAATA TCCAAGGTAA AAACTACAAT AGCGGCATAC TCGCCGTCGA
201 TAATATGCC GTTGTTAAGA AATATATTAC AGATACTTAC GGGGATAATT
251 TAAAGGATGC GGTAAAGAAG CAATTACAGG ATTTATACAA ACAAAGACCC
301 GAAGCTTGGG AAGAAAATAA AAAACGGACT GAGGAGCGT ATATAGAAC
351 GCTTGGACCA AAATTTAGTA TACTCAAAC AAAAAACCCC GATTTAATT
401 ATAAATTGGT AGAAGATTCC GTACTCACTC CTCATAGTAA TACATCACAG
451 ACTAGTCTCA ACAACATCTT CAATAAAAAA TTACACGTCA AAATCGAAAA
501 CAAATCCCAC GTGCCCGGAC AGGTGTTGGA ACTGACCAAG ATGACGCTGA
551 AAGATTCCCT TTGGGAACCG CGCCGCCATT CCGACATCCA TATGCTGGAA
601 ACTTCCGATA ATGCCCGCAT CGCCTGAAC ACGAAAGATG AAAAATGAC
651 CGTCCATAAA GCGTATCAGG GCGGTGCGGA TTTCTGTTC GGCTACGACG
701 TGCAGGGAGTC GGACAAACCC GCCCTGACCT TTGAAGAAAA AGTCAGCGGA
751 CAATCCGGCG TGTTTTGGG ACGCCGGCCG GAAAATCTGA AAACGCTCGA
801 CGGGCGCAAA CTGATTGCGG CGGAAAAGGC AGACTCTAAT TCGTTTGCGT
851 TTAAACAAAAA TTACCGGGCAG GGACTGTACG ATTATTGCT CAAGCAATGC
901 GAAGGGCGAT TTTGCTTGGG CGTGCAGCGT TTGGCTATCC CCGAGGCGGA
951 AGCGGTTTTA TATGCCAAC AGGCTTATGC GGCCTTAACT TTGTTCGGGC
1001 TGCCTGCCGC CGACAGGGGC GACGACGTGT ATGCCGCCGA TCCGTCGGCGT
1051 CAAAAATTGT GGCTGCGCTT CATCGGCCGC CGCTCGCATC AAAATATACG
1101 GGGCGCGCG GCTGCGGACG GGCAGCGCAA AGGCGTCAA ATCGGCGGGC
1151 AGGTGTTGT ACGGCAAAAT GAAGGCAGCC GGCTGGCAAT CGGCGTGATG
1201 GGCAGGCGAGG CTGGCCAGCA CGCATCAGTC AACGGCAAAG GCGGTGCGGC
1251 AGGCAGTTAT TTGCATGGTT ATGGCGGGGG TGTTTATGCT GCGTGGCATC
1301 AGTTGCGCGA TAAACAAACG GGTGCGTATT TGGACGGCTG GTTGAATAC
1351 CAAACGTTCA AACACCGCAT CAATGATGAA AACCGCTGCGG AACGCTACAA
1401 AACCAAAAGGT TGGACGGCTT CTGTCGAAGG CGGCTACAAC GCGCTTGTTG
1451 CGGAAGGGGT TGTCGGAAAA GGCAATAATG TGCGGTTTTA CCTGCAACCG
1501 CAGGGCGCAGT TTACCTACTT GGGCGTAAAC GGCGCTTTA CCGACAGCGA
1551 GGGGACGGCG GTCGGACTGC TCAGTGGCAA AGCCGCGCCG
1601 GCATTGGGC AAAAACCCGT TTTGCTTGC GTAACGGTGT CAATCTTCAG
1651 CCTTTGCGC CTTTTAATGT TTTGCACAGG TCAAAATCTT TCGGCGTGGG
1701 AATGGACGGC GAAAAAACAGA CGCTGGCAGG CAGGACGGCG CTCGAAGGGC
1751 GGTTCGGCAT TGAAGCCGGT TGGAAAGGCC ATATGTCCGC ACGCATCGGA
1801 TACGGCAAA GGACGGACGG CGACAAAGAA GCCGCATTGT CGCTCAAATG
1851 GCTGTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2994; ORF 990.a>:

a990.pep

```

1 MFRAQLGSNT RSTKIGDDAD FSFSDKPKPG TSHYFSSGKT DQNSSEYGYD
51 EINIQGKNYN SGILAVDNMP VVKKYITDTY GDNLKDAVKK QLQDLYKTRP
101 EAWEENKKRT EEAYIEQLGP KFSILKQKNP DLINKLVEDS VLTPHSNTSQ
151 TSLNNIFNKK LHVKIENKSH VAGQVLELTK MTLKDSLWEP RRHSDIHMLE
201 TSDNARIRLN TKDEKLTVHK AYQGGADFLF GYDVRESDKP ALTFEEKVSG
251 QSGVVLERRP ENLKTLGDRK LIAAEKADSN SFAFKQNYRQ GLYELLLKQC
301 EGGFCLGVQR LAIPEAEAVL YAQQAYAAANT LFGLRAADRG DDVYAADPSR
351 QKLWLRFIGG RSHQNIRGGA AADGRRKGVQ IGGEVFVRQN EGSRLAIGVM

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1409

401	GGRAGQHASYV	NGKGGAAAGSY	LHGYYYYVYA	AWHQLRDKQT	GAYLDGWLQY
451	QRFKHRINDE	NRAERYKTKG	WTASVEGGYN	ALVAEGVVGK	GNNVRFLYLPQ
501	QAQFTYLGVN	GGFTDSEGT	VGLLGSGQWQ	SRAGIRAKTR	FALRNGVNLF
551	PFAAFNVLHR	SKSFGVEMDG	EKQTLAGR	TELEGRFGIEAG	WKGHMSARIG
601	YGKRTDGDKE	AALSLKWLF*			

m990/a990 96.0% identity in 619 aa overlap

	10	20	30	40	50	60
m990.pep	MFRAQLGSNTRSTKIGDDADFSFSDKPKPGTSHYFSSGKTDQNSSEYGYDEINIQGKNY					
a990	MFRAQLGSNTRSTKIGDDADFSFSDKPKPGTSHYFSSGKTDQNSSEYGYDEINIQGKNY	10	20	30	40	50
m990.pep	SGILAVDNMPVVKYITEKYGADLKQAVKSQQLQDLYKTRPEAWAENKKRTEEAYIAQFGT	70	80	90	100	110
a990	SGILAVDNMPVVKYITDTYGDNLKDAVKKQLQDLYKTRPEAWEENKKRTEEAYIEQLGP	70	80	90	100	110
m990.pep	KFSTLQTKMPDPLINKLVEDSVLTPHSNTSQTSLNNIFNKKLHVKIEENKSHVAGQVLELT	130	140	150	160	170
a990	KFSILKQKQNPDPLINKLVEDSVLTPHSNTSQTSLNNIFNKKLHVKIEENKSHVAGQVLELT	130	140	150	160	170
m990.pep	MTLKDSLWEPRRHSDIHTLETSDNARIRLNKDEKLTVHKDYAGGADFLFGYDVRESDEP	190	200	210	220	230
a990	MTLKDSLWEPRRHSDIHMLETSDNARIRLNKDEKLTVHKAYQGGADFLFGYDVRESDKP	190	200	210	220	230
m990.pep	ALTFEDKVSGQGVVLERRPENLKTLDGRKLIAAKTADSGSFAFKQNYRQGLYELLLKQC	250	260	270	280	290
a990	ALTFEEKVSGQGVVLERRPENLKTLDGRKLIAAEKADNSNSFAFKQNYRQGLYELLLKQC	250	260	270	280	290
m990.pep	EGGFCLGVQRЛАIPEAEAVLYAQQAAYAANTLFGLRAADRGDDVYADPSRQKLWLRFIGG	310	320	330	340	350
a990	EGGFCLGVQRЛАIPEAEAVLYAQQAAYAANTLFGLRAADRGDDVYADPSRQKLWLRFIGG	310	320	330	340	350
m990.pep	RSHQNIRGAAADGWRKGVQIGGEVFRQNEGSRLAIGVMGGAGQHASVNGKGGAAAGSD	370	380	390	400	410
a990	RSHQNIRGAAADGRRKGVQIGGEVFRQNEGSRLAIGVMGGAGQHASVNGKGGAAAGSY	370	380	390	400	410
m990.pep	LYGYGGGVYAAWHQLRDQGTGAYLDGWLQYQRFKHRINDENRAERYKTKGWTASVEGGYM	430	440	450	460	470
a990	LHGYGGGVYAAWHQLRDQGTGAYLDGWLQYQRFKHRINDENRAERYKTKGWTASVEGGYM	430	440	450	460	470
m990.pep	ALVAEGIVGKGNNVRFLQPKAQFTYLGVNNGFTDSEGTAVGLLGSGQWQSRAKIRAKT	490	500	510	520	530
a990	ALVAEGVVGKGNNVRFLQPKAQFTYLGVNNGFTDSEGTAVGLLGSGQWQSRAKIRAKT	490	500	510	520	530
m990.pep	FALRNGVNLPFAAFNVLHRSKSFVEMDGEKQTLAGRATLEGRFGIEAGWKGHMSARI	550	560	570	580	590
a990	FALRNGVNLPFAAFNVLHRSKSFVEMDGEKQTLAGRATLEGRFGIEAGWKGHMSARI	550	560	570	580	590

1410

	550	560	570	580	590	600
	610	620				
m990.pep	YGKRTDGDKEAALSLKWLFX 					
a990	YGKRTDGDKEAALSLKWLFX 610 620					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2995>:

g992.seq

```

1 ATGTTAGAC GGCATCGGCA TTTGAAAAAT ATGCAGATTA AAAAAATCAT
51 GAAATGGCTT CCCGTCGCCC TGTCGCTTT GGGCGCGTTG GGTTATACGG
101 GATATGACAG TGAGGCAGTG CGGACGGCGG TTGCGGTACT CGACGTACTC
151 GGCACACTGAG GGGACGTGGG TTTCGACCGG CCGCTTCGCC GACGGGCATC
201 GGCAGAAATCC GCCCACAGCT ACACAGGCAC GGTGTCCAAA GTCTATGACG
251 GCGATACCCCT TCACGTCATC GACGGCGAGC GCGCGAAACA TAAAATTGCG
301 ATGGCGTATA TCGACGCCACC GGAGATGAAA CAGGCTTACG GTACACGTTG
351 GCGCGACAACT CTGCGCGCGG CGGCAGGAGGG TAGGAAAGTC AGTGTACGTG
401 TGTGAAAC CGACCGCTAT CAGCGCGAAG TGCGCGAGGT ATCCGCCGGC
451 AAAACCGATT TGAACCTGAT GCAGGTGCAG GACGGGGCGG CGTGGCATTA
501 TAAAAGTTAT GCTAAAGAAC AGCAGGATAA GGCAGGATTT GCGCACTATG
551 CCGACGCTCA ATTCAAGCG GAAAGGGAAC GCAAAGGATT GTGGAAAGCT
601 AAAAATCCGC AAGCGCGTG GGCGTACCGC CGGGCAGGCA GGAGCGGCAGG
651 GGGCAATAAG GATTGGATGG ATTCCGTGGG CGAATGGTTG GGCATTGGT
701 AA

```

This corresponds to the amino acid sequence <SEQ ID 2996 ORF 992.ng>:

g992.pep

```

1 MFRRHRHLKN MQIKKIMKWL PVALSLLGAL GYTGYDSEAV RTAVAVLDVL
51 GTAGDVGFDA PVRRAASAKS GHSYTGTVS K VYDGDTLHVI DGDGAKHKIR
101 MAYIDAPEMK QAYGTRS RDN LRAAAEGRKV SVRVFETDRY QREVAQVSAG
151 KTDLNLMQVQ DGAAWHYKS AKEQODKADF ADYADAQIQA ERERKGLWKA
201 KNPQAPWAYR RAGRSGGGNK DWMDSVGEWL GIW*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2997>:

m992.seq

```

1 ATGTTAGAC GGCATCGGCA TTTGAAAAAT ATGCAGATTA AAAAAATCAT
51 GAAATGGCTT CCCGTCGCCC TGTCGCTTT GGGCGCGTTG GGTTATACGG
101 GGTACGGAG CGAGGCAGTG CGGACGGCGG TTGCGGTACT CGACGTACTC
151 GGCAGGGCAG GGGACGCGGG TTCCGACCGC CCGCCCGGCC GCGGAGCATE
201 GGCAGAAATCC GCCCACCGCT ACACAGGCAC GGTGTCCAAA GTCTATGACG
251 GCGACACCCT TCACGTTATC GACGGCGACG CGCGAAACA CAAAATCCGG
301 ATGGCGTATA TCGACGCCGCC GGAGATGAAA CAGGCTTACG GCACCGTTG
351 GCGCGACAACT CTGCGCGCGG CGGCAGGAGGG CAGGAAAGTC AGCCTGCGCG
401 TGTGCGATAC CGACCGCTAC CAGCGCGAAG TGCGCGAGGT TTCTGTCGGC
451 AAAACCGATT TGAACCTGAT GCAGGTGCAG GACGGGGCGG CGTGGCATTA
501 TAAAAGTTAT GCTAAAGAAC AGCAGGATAA GGCAGGATTT GCGGATTATG
551 CCGACGCTCA ATTCAAGCG GAAAGGGAAC GCAAAGGATT GTGGAAAGCT
601 AAAAATCCGC AAGCGCGTG GGCGTACCGC CGAGCAGGCA GGAGCGGCAGG
651 GGGCAATAAG GATTGGATGG ATGCCGTGGG CGAATGGTTG GGCATTGGT
701 AA

```

This corresponds to the amino acid sequence <SEQ ID 2998; ORF 992>:

m992.pep

```

1 MFRRHRHLKN MQIKKIMKWL PVALSLLGAL GYTGYGSEAV RTAVAVLDVL
51 GAAGDAGSDA PARRASAKS GHRYTGTVS K VYDGDTLHVI DGDGAKHKIR
101 MAYIDAPEMK QAYGTRS RDN LRAAAEGRKV SVRVFETDRY QREVAQVSAG
151 KTDLNLMQVQ DGAAWHYKS AKEQODKADF ADYADAQIQA ERERKGLWKA
201 KNPQAPWAYR RAGRSGGGNK DWMDAVGEWL GIW*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 992 shows 96.1% identity over a 233 aa overlap with a predicted ORF (ORF 992) from *N. gonorrhoeae*

m992/g992 96.1% identity in 233 aa overlap

1411

	10	20	30	40	50	60
m992.pep	MFRRHRHLKNMQIKKIMKWLPVALSLLGALGYTGYGSEAVRTAVAVLDVLGAAGDAGSDA : :					
g992	MFRRHRHLKNMQIKKIMKWLPVALSLLGALGYTGYDSEAVRTAVAVLDVLGTAGDVGFD 10 20 30 40 50 60					
	70	80	90	100	110	120
m992.pep	PARRRASAKSGHRYTGTGVSKVYDGDTLHVIDGDGAKHHKIRMAYIDAPEMKQAYGTRSRDN : : : :					
g992	PVRRRASAKSGHSYTGTGVSKVYDGDTLHVIDGDGAKHHKIRMAYIDAPEMKQAYGTRSRDN 70 80 90 100 110 120					
	130	140	150	160	170	180
m992.pep	LRAAAEGRKVSVRVFDTDRYQREVAQVSVGKTDLNLMQVQDGAAWHYKSYAKEQQDKADF : : : :					
g992	LRAAAEGRKVSVRVFETDRYQREVAQVSACKTDLNLMQVQDGAAWHYKSYAKEQQDKADF 130 140 150 160 170 180					
	190	200	210	220	230	
m992.pep	ADYADAQIQAERERKGLWKAQNPQAPWAYRRAGRSGGGNNDWMDAVGEWLGIWX : : :					
g992	ADYADAQIQAERERKGLWKAQNPQAPWAYRRAGRSGGGNNDWMDSVGEWLGIWX 190 200 210 220 230					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2999>:

a992.seq

```

1 ATGTTCAGAC GGCATCGGCA TTGAAAAAT ATGCAGATA AAAAAATCAT
51 GAAATGGCTT CCCGTCGCT TGTCGCTTTT GGGTGCCTTG GGTTATACGG
101 GGTACGGCAG CGAGCGGTG CGGACGGCGG TTGCCGTACT CGACGTACTC
151 GGCAGCCGAG GGGACGCGGG TTCCGACGCG CCGGCCCCGCC GCGGAGCCATC
201 GGCAGAAATCC GGCCACCGCT ACACAGGCAC GGTGTCCAAA GTCTATGACG
251 GCGACACCC CTACCGTATC GACGGCGACG GCGCGAAACA CAAATCCGG
301 ATGGCGTATA TCGACGCCGC GGAGATGAAA CAGGCTTACG GCACCGCTTC
351 GCGCGACAC CTGCGCGCGG CGCGGGAAGG CAGGAAAGTC AGCGTCCCGCG
401 TGTTCGACAC CGACCGCTAC CAGCGCGAAG TGGCCGAGGT TTCTGTCCGC
451 AAAACCGATT TGAACCTGAT GCAAGGTGCGAG GACGGGGCGGG CGTGGCATTAA
501 TAAAGATTAT GCTAAAGAAC AGCAGGATAA GGCGGATTTT GCCGATTATG
551 CCGACGCTCA ATTACAGCGG GAAAGGGAAC GCAAAGGATT GTGGAAAGCT
601 AAAATCCGC AAGCGCCGTG GGGTACCGC CGGGCAGGCCA GGAGCGGC
651 GGGCAATAAG GATTGGATGG ATGCCGTGGG CGAATGGTTG GGCATTTGGT
701 AA

```

This corresponds to the amino acid sequence <SEQ ID 3000; ORF 992.a>:

a992.pep

```

1 MFRRHRHLKN MQIKKIMKWL PVALSLLGAL GYTGYGSEAV RTAVAVLDVL
51 GAAGDAGSDA PARRRASAKS GHRYTGTGVSK VYDGDTLHV DGDGAKHHKIR
101 MAYIDAPEMK QAYGTRSRDN LRAAAEGRKV SVRVFDTDRY QREVAQVSVG
151 KTDLNLMQVQ DGAAWHYKSY AKEQQDKADF ADYADAQIQA ERERKGLWKA
201 KNPQAPWAYR RAGRSGGGNK DWMDAVGEWL GIW*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 992 shows 100.0% identity over a 233 aa overlap with a predicted ORF (ORF 992) from *N. meningitidis*

a992/m992 100.0% identity in 233 aa overlap

	10	20	30	40	50	60
a992.pep	MFRHRHLKNMQIKKIMKWL PVALSLLGAL GYTGYGSEAVRTAVAVLDVLGAAGDAGSDA :					
m992	MFRHRHLKNMQIKKIMKWL PVALSLLGAL GYTGYGSEAVRTAVAVLDVLGAAGDAGSDA 10 20 30 40 50 60					
	70	80	90	100	110	120
a992.pep	PARRRASAKSGHRYTGTGVSKVYDGDTLHV IDGDGAKHHKIRMAYIDAPEMKQAYGTRSRDN : :					
m992	PARRRASAKSGHRYTGTGVSKVYDGDTLHV IDGDGAKHHKIRMAYIDAPEMKQAYGTRSRDN 70 80 90 100 110 120					
	130	140	150	160	170	180

a992.pep	LRAAAEGRKVSERVFDTDYQREVAQSVGKTDLNLMQVQDGAAWHYSYAKEQQDKADF 					
m992	LRAAAEGRKVSERVFDTDYQREVAQSVGKTDLNLMQVQDGAAWHYSYAKEQQDKADF 130 140 150 160 170 180					
a992.pep	190	200	210	220	230	
m992	ADYADAQIQAERERKGLWKAKNPQAPWAYRAGRSGGGNKDWMDAVGEWLGIWX 190 200 210 220 230					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3001>:

g993.seq

```

1 CTGAAAGTCG TATTGGGCAG TTTCAAGGC CCTTTGGATC TGCTGCTCTA
51 CTTTATCCGC AAGCAGAAC TCGATGTTCT CGATATTCCG ATGGTGAAA
101 TTACCGGGCA GTATCTGCAC TATATTGCCA AAATGGAAGC CTATCAGTT
151 GATTTGGCGG CGGAATATCT TTGATGGCG GCAATGCTGA TTGAAATCAA
201 ATCGCGCTCG CTGCTGCCGC GTACCGAAGC CGTCGAAGAC GAAGAGGCCG
251 ACCCGCGTGC CGAGTTGGTG CGCCGTCTGC TTGCTACGA GCAAATGAAA
301 CTGGCGGGCG AGGGTTTGGG CGCGCTGCCG CGTGCAGGAC GGGATTCGGC
351 GTGGGCTTAC CTGCCGCTGG AAATTGCAGC CGAGACGAAG CTGCCCAGG
401 TTACATCGC CGATTGATG CAGGCATGGT TGGGCATTCT TTCTCGGGCA
451 AACATACGC CGAGCCACGA AGTAATCCAA GAAACCCCTT CCGTGCAGGC
501 GCAAATGACG GCAATCTGC CGCGTTTGAA CGAACACGGG ATATGCAGGT
551 TTCACGCCCT GTTCAATCCC GAAACAGGGCG CGGCTTACGT GATCGTCAAC
601 TTCATCGCCC TGTTGGAGCT TGCCAAAGAA GGATTGGTCG GAATCGTACA
651 GGAAGACGGT TTCGGAGAAA TCCGAATCAG CCTCAATCAT GAGGGGGCGC
701 ATTCAAGACGG CATTTCGGC ACACGGGGCG GGCAGATGT GTTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 3002 ORF 993.ng>:

g993.pep

```

1 LKVVLGSFQG PLDLLLLYLIR KQNIDVLDIP MVEITGQYLH YIAQMEAYQF
51 DLAAEYLLMA AMLIEIKSRL LLPRTEAVED EEAAPRAELV RRLLAYEQMK
101 LAAQQLDALP RAGRDFAWAY LPLEIAAEK LPEVYIADLM QAWLGILSRA
151 KHTRSHEVIQ ETISVRAQMT AILRRRNHEHG ICRFHDLFNP EQGAAYVIVN
201 FIALLELAKE GLVGIVQEDG FGEIRISLNH EGAHSDGIFG TRGGRDVF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3003>:

m993.seq

```

1 TTGAAAGTCG TATTGGGCAG CTTCCAAGGC CCTTTGGATC TACTGCTGTA
51 TCTGATCCGC AAACAGAAATA TCGACGTACT GGATATTCCG ATGGTGAAGA
101 TTACCGGGCA GTATCTGCAC TACATGCCGC AAATAGAAAC CTATCAGTT
151 GATTTGGCGG CGGAATATCT TTGATGGCA GCAATGCTGA TTGAAATCAA
201 ATCGCGCTCG CTGCTGCCGC GTACCGAAC CGTCGAAGAC GAAGAAGCCG
251 ACCCGCGTGC CGAGTTGGTG CGCCGCTGC TGGCTTACGA ACAGATGAAG
301 CTGGCGGGCG AGGGTTTGGG CGCGCTGCCG CGAGCCGGAC GGGATTCGGC
351 GTGGGCTTAC CTGCCGCTGG AAATTGCCGT CGAAGCCAAG CTGCCCCAAG
401 TCTATATTAC CGACTTGACG CAAGCGTGGC TGGGTATTTT GTCTCGGGCA
451 AACACACACG GCAAGCCACGA AGTAATCAA GAAACCATCT CCCTGCGCGC
501 GCAAATGACG GCAATCTGC CGCGTTTGAA CGGACACGGG ATATGCAGGT
551 TTCACGACCT GTTCAATCCC AAACAGGGCG CGGCTTACGT GGTCGTCAAC
601 TTCATCGCAC TGTTGGAGCT TGCCAAAGAA GGATTGGTCG GAATCGTGC
651 GGAAGACGGT TTCGGAGAAA TCCGAATCAG CCTCAATCAT GAGGGGGCGC
701 ATTCAAGACGG CATTTCGGC ACACGGGGCG GGCAGATGT GTTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 3004; ORF 993>:

m993.pep

```

1 LKVVLGSFQG PLDLLLLYLIR KQNIDVLDIP MKVITEQYLH YIAQIETYQF
51 DLAAEYLLMA AMLIEIKSRL LLPRTEAVED EEAAPRAELV RRLLAYEQMK
101 LAAQQLDALP RAGRDFAWAY LPLEIAAEK LPEVYIADLM QAWLGILSRA
151 KHTRSHEVIQ ETISVRAQMT AILRRRNHEHG ICRFHDLFNP KQGAAYVVVN
201 FIALLELAKE GLVRIVQEDG FGEIRISLNH EGAHSDGIFG TRGGRDVF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 993 shows 93.1% identity over a 248 aa overlap with a predicted ORF (ORF 993) from *N. gonorrhoeae*

m993/g993 93.1% identity in 248 aa overlap

	10	20	30	40	50	60
m993.pep	LKVVLSFQGPLDLLLLLIRKQNIDVLDIPMVKITEQYLHYIAQIETYQFDLAAEYLLMA					
g993	: : : : : : : : : : : LKVVLSFQGPLDLLLLLIRKQNIDVLDIPMVMEITGQYLHYIAQMEAYQFDLAAEYLLMA					
	10	20	30	40	50	60
m993.pep	70 80 90 100 110 120					
g993	AMLIEIKSRLLLLPRTEAVEDEEADPRAELVRRLLAYEQMKLAAQGLDALPRAGRDFAWAY : : : : : : : : : : : AMLIEIKSRLLLLPRTEAVEDEEADPRAELVRRLLAYEQMKLAAQGLDALPRAGRDFAWAY					
	70	80	90	100	110	120
m993.pep	130 140 150 160 170 180					
g993	LPLEIAVEAKLPEVYITDLTQAWLGILSRRAKHTRSHETIKETISVRAQMTAILRRLNHG : : : : : : : : : : LPLEIAAAETKLPEVYIADLMQAWLGILSRRAKHTRSHETIQETLSVRAQMTAILRRLNHG					
	130	140	150	160	170	180
m993.pep	190 200 210 220 230 240					
g993	ICRFHDLFNPQGAAYVVVNFIALLELAKEGLVРИVQEDGFGEIRISLNHEGAHSDGISM : : : : : : : : ICRFHALFNPEQGAAYVIVVNFIALLELAKEGLVGIVQEDGFGEIRISLNHEGAHSDGIFG					
	190	200	210	220	230	240
m993.pep	249					
g993	TRGGRDVFX : TRGGRDVFX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3005>:

a993.seq

```

1 CTGAAAGTCG TATTGAGCAG TTTCAAGGC CCTTTGGATC TGCTGCTCTA
51 CCTTATCCG AAGCAGAAC TCGATGTTCT CGATATTCCG ATGGTGAAGA
101 TTACCGAAC A GTATCTGCAC TACATCGCCC AAATAGAAC CTATCAGTT
151 GATTGGCGG CGGAATATCT TTTGATGGCA GCAATGCTGA TTGAAATCAA
201 ATCGCGCTG CTGCTGCCGC GTACCGAAAC CGTCGAAGAC GAAGAAGCCG
251 ACCCGCGTGC CGAGTTGGTG CGCCGCTGC TGGCTTACGA GCAGATGAAG
301 CTGGCGGCAC AAGGGTTGGA TGCCCTTCCT CCGTGCAGGCC GGGATTTCGC
351 ATGGGCATAC CTGCCACTGG AAATGCCGT CGAAGCCAAG CTGCCCGAAG
401 TCTATATTAC CGACTTGACG CAGCGTGGC TGAGTATTTT GTCTCGGGCA
451 AAACATACCG GCAGCCACGA ACTTATCAAA GAAACCATCT CCGTGCAGCGC
501 GCAAATGACG GCAATCCTGC GCCGTTGAA CAAACACGGG ATATGCAGGT
551 TTCACGACCT GTTCAATCCC GAACAGGGCG CCGCTTACGT GGTCGTCAAC
601 TTCACTGCAC TGTTGGAGCT TGCCAAAGAA GGTTTGGTCG GAATCGTACA
651 GGAAGTCGGT TTCTGGAGAAA TCCGAATCAG CCTCAATCAT GAGGGGGCGC
701 ATTCAAGACGG CATTCCGGC ACACGGGGCG GGCAGATGT GTTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 3006; ORF 993.a>:

a993.pep

```

1 LKVVLSSFQG PLDLLLLLIR KQNIDVLDIP MVKITEQYLH YIAQIETYQF
51 DLAAEYLLMA AMLIEIKSRL LLPRTETVED EADPRAELV RRLLAYEQMK
101 LAAQGLDALP RAGRDFAWAY LPLEIAVEAK LPEVYITDLT QAWLSILSRA
151 KHTRSHETIK ETISVRAQMT AILRRLNKHG ICRFHDLFNP EQGAAYVVVN
201 FIALLELAKE GLVGIVQEVG FGEIRISLNH EGAHSDGISM TRGGRDVFX*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 993 shows 97.6% identity over a 248 aa overlap with a predicted ORF (ORF 993) from *N. meningitidis*

a993/m993 97.6% identity in 248 aa overlap

	10	20	30	40	50	60
a993.pep	LKVVLSFQGPLDLLLLLIRKQNIDVLDIPMVKITEQYLHYIAQIETYQFDLAAEYLLMA					
m993	: : : : : : : : : LKVVLSFQGPLDLLLLLIRKQNIDVLDIPMVKITEQYLHYIAQIETYQFDLAAEYLLMA					

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	10	20	30	40	50	60
a993.pep	70	80	90	100	110	120
m993	AMLIEIKSRLLLPRTETVEDEEADPRAELVRRLLAYEQMKLAAQGLDALPRAGRDFAWAY 70	80	90	100	110	120
a993.pep	130	140	150	160	170	180
m993	PLEIAVEAKLPEVYITDLTQAWLSILSRALKHRSHEVIKETISVRAQMATAILRRLNKHG 130	140	150	160	170	180
a993.pep	190	200	210	220	230	240
m993	ICRFHDLFNPQEQQAAAYVVVNFIALLELAKEGLVGVQEVGFGEIRISLNHEGAHSDGISM 190	200	210	220	230	240
a993.pep	249	TRGGGRDVFX				
m993	TRGGGRDVFX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3007>:

g996.seq

```

1 ATGAACAGAA GAACCTTCCT CCTCGCGC GA CGCGTTGC TTCTTACCGC
51 CTGGCGAGA AAATCCGCC GAACCCACGC CAAAATTCCC GAAGGAAGCA
101 CCGTGCTTGC CTTGGGGCAT TCGCTCACCT TCGGCTACGG AGCAAACCCC
151 GGCGAATCCT ACCCCGCGCA ACTGCAAAAA CTGACGGGTT GGAATATTGT
201 CAACGGCGGC GTATCGGGC ATACGTCGC GCAAGCCCTA TCGCGCCTGC
251 CCGCGCTGTT GGCACGCAA CCCAACGCTTG TGATTGTCGG CATAGGCGGC
301 AACGACTTTC TGCGCAAAGT TCCCGAGGAG CAGACCCCGG CCAATATCGC
351 GAAAATCATC GAAACCGTGC AAAAGGAAAA CATTCCCGCC GTCCCTGTCG
401 GCGTGCCGCA CATCACACTG GGCACGTTGT TCGGGCATTG GAGCGACCAT
451 CCGCTGTATG AGGATTGTC CGAGGAATAC GGCATTCCGT TGTCGGCGG
501 CGCGTGGCG GAAATTGTC GCGATAATAA TCTGAAATCC GACCAAATCC
551 ACGCCAACGG CAAAGGCTAT CGGAAATTG CGGAAATTT GAATCAATT
601 TTGAGAAAAC ATGGGTTTAG ATAA

```

This corresponds to the amino acid sequence <SEQ ID 3008 ORF 996.ng>:

g996.pep

```

1 MNRRTFLLGA GALLTACGR KSARTHAKIP EGSTVLALGD SLTFGYGANP
51 GESYPAQLQK LTGWNIVNGG VSGDTSAQAL SRLPALLARK PKLVIVGIGG
101 NDFLRKVPEE QTRANIAKII ETVQKENIPA VLVGVPHTL GALFGHLSDH
151 PLYEDLSEEEY GIPLFGGAWA EILGNNNLKS DQIHANGKGY RKFAENLNQF
201 LRKHGER*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3009>:

m996.seq

```

1 ATGAACAGAA GAACCTTCCT CCTCGCGC GA CGCGTTGC TGCTTACCGC
51 CTGGCGAGA AAATCCGCC GAACCCACGC CAAAATTCCC GAAGGAAGCA
101 CCGTACTTGC CTTGGGGCAT TCGCTTACCT TCGGCTACGG CGCAAACCCC
151 GGCGAATCCT ACCCCGCGCA ACTGCAAAAA CTGACGGGTT GGAATATTGT
201 CAACGGCGGC GTATCGGGC ATACATCTGC CCAAGCCCTG TCGCGCCTGC
251 CCGCGCTGTT GGCACGCAA CCCAACGCTTG TGATTGTCGG CATAGGCGGC
301 AACGACTTTC TGCGCAAAGT TCCCGAGGAG CAGACCCCGG CCAATATCGC
351 GAAAATCATC GAAACCGTGC AGAAGGAAAA CATTCCCGCC GTCCCTGTCG
401 GCGTGCCGCA CATCACACTG GGTGCACGTTGT TCGGGCATTG GAGCGATCAT
451 CCGCTGTATG AGGATTGTC CGAGGAATAC GGCATTCCGT TGTCGGCGG
501 CGCGTGGCG GAAATTGTC GCGATAATAA TCTGAAATCC GACCAAATCC
551 ACGCCAACGG CAAAGGCTAT CGGAAATTG CGGAAAGATTG GAATCAATT
601 TTGAGAAAAC AGGGGTTTAG ATAA

```

This corresponds to the amino acid sequence <SEQ ID 3010; ORF 996>:

m996.pep

```

1 MNRRTFLLGA GALLTACGR KSARTHAKIP EGSTVLALGD SLTFGYGANP
51 GESYPAQLQK LTGWNIVNGG VSGDTSAQAL SRLPALLARK PKLVIVGIGG

```

101 NDFLRKVPKE QTRANIAKII ETVQKENIPA VLGVGVPHITL GALFGHLSDH
 151 PLYEDLSEEEY GIPLFGGAWA EILGDNNLKS DQIHANGKGY RKFAEDLNQF
 201 LRKQGFR

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 996 shows 98.1% identity over a 207 aa overlap with a predicted ORF (ORF 996) from *N. gonorrhoeae*

m996/g996 98.1% identity in 207 aa overlap

m996.pep	10 20 30 40 50 60
	MNRRTFLLGAGALLTACGRKSARTHAKIPEGSTVLALGDSLTFGYGANPGESYPAQLQK
g996	10 20 30 40 50 60
	MNRRTFLLGAGALLTACGRKSARTHAKIPEGSTVLALGDSLTFGYGANPGESYPAQLQK
m996.pep	70 80 90 100 110 120
	LTGWNIVNGGVSGDTSAQALSRLPALLARKPKLVIVGIGNDFLRKVPKEQTRANIAKII
g996	70 80 90 100 110 120
	LTGWNIVNGGVSGDTSAQALSRLPALLARKPKLVIVGIGNDFLRKVPEEOTRANIAKII
m996.pep	130 140 150 160 170 180
	ETVQKENIPAVLVGVPHITLGAFLGHLSDHPLYEDLSEEEYGIPLFGGAWAEILGDNNLKS
g996	130 140 150 160 170 180
	ETVQKENIPAVLVGVPHITLGAFLGHLSDHPLYEDLSEEEYGIPLFGGAWAEILGNNNLKS
m996.pep	190 200
	DQIHANGKGYRKFAEDLNQFLRKQGFR
g996	190 200
	DQIHANGKGYRKFAENLNQFLRKHGFRX

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3011>:

a996.seq

```

1 ATGAACAGAA GAACCTTCCT CCTCGGCGCA GGCAGCTTGC TCCTTACCGC
 51 CTGGCGAGA AAATCCGCC GAACCCACGC CAAAATTCCC GAAGGAAGCA
101 CCGTACTTGC CTTGGGGAT TCGCTTACCT TCGGCTACGG CGCAAACCCC
151 GGCGAATCTC ACCCCCGCGCA ACTGAAAAAA CTGACGGGTG GGAATATTGT
201 CAACGGCGGC GTATCGGGCG ATACATCCGC CCAAGCCCTG TCGCGCCTGC
251 CCGCGCTGTT GGCACCCAAA CCCAAGCTTG TGATTGTCGG CATAAGGGCG
301 AACGACTTTC TGCGCAAAAGT TCCAAGGGAG CAGACCCCGC CCAATATCGC
351 GAAAATCATC GAAACCGTGC AGAAGGAAAA CATCCCCGCC GTCCTCGTCG
401 GCGTGGCGCA CATTACCTTG GGCAGCTTGT TCGGGCATTG GAGCGATCAT
451 CGCGTGTATG AGGATTGTC CGAGGAATAC GGCATTCCGC TGTCGGCGG
501 CGCGTGGGGCG GAAATTGTTGG GCGATAATAA TCTGAAATCC GACCAAATCC
551 ACGCCAACGG CAAAGGCTAT CGGAAATTG CCGAAGATTG GAATCAATT
601 TTGAGAAAAC AGGGTTTAG ATAA

```

This corresponds to the amino acid sequence <SEQ ID 3012; ORF 996.a>:

a996.pep

```

1 MNRRTFLLGA GALLTACGR KSARTHAKIP EGSTVLALGD SLTFGYGANP
 51 GESYPAOLQK LTGWNIVNGG VSGDTSAQAL SRLPALLARK PKLVIVGIGG
101 NDFLRKVPKE QTRANIAKII ETVQKENIPA VLGVGVPHITL GALFGHLSDH
151 PLYEDLSEEEY GIPLFGGAWA EILGDNNLKS DQIHANGKGY RKFAEDLNQF
201 LRKQGFR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 996 shows 100.0% identity over a 207 aa overlap with a predicted ORF (ORF 996) from *N. meningitidis*

a996/m996 100.0% identity in 207 aa overlap

a996.pep	10 20 30 40 50 60
	MNRRTFLLGAGALLTACGRKSARTHAKIPEGSTVLALGDSLTFGYGANPGESYPAQLQK

m996	MNRRTFLLGAGALLTACGRKSARTHAKIPEGSTVLALGDSLTFGYGANPGESYPAQLQK 10 20 30 40 50 60
a996.pep	LTGWNIVNGGVSGDTSAQALSRLPALLARKPKLVIVGIGGNDFLRKVPKEQTRANIAKII 70 80 90 100 110 120
m996	LTGWNIVNGGVSGDTSAQALSRLPALLARKPKLVIVGIGGNDFLRKVPKEQTRANIAKII 70 80 90 100 110 120
a996.pep	ETVQKENIPAVLGVGVPHITLGALFGHLSDHPLYEDLSEEYGIPLFGGAWAEILGDNNLKS 130 140 150 160 170 180
m996	ETVQKENIPAVLGVGVPHITLGALFGHLSDHPLYEDLSEEYGIPLFGGAWAEILGDNNLKS 130 140 150 160 170 180
a996.pep	DQIHANGKGYRKFAEDLNQFLRKQGFRX 190 200
m996	DQIHANGKGYRKFAEDLNQFLRKQGFR 190 200

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3013>:

g997.seq (partial)

1	ATGATGAACA	CGCCGCATCC	GCGCCCGAAA	ATCGCGTCA	TGGCGCAGG
51	CTGGGCCGGC	TTGTCCGGCG	CGTCACCTT	GGCGCGGCAC	GCCGACGTTA
101	CCCTGTTTGA	AGCCGGCCGG	CAGGGGGCG	GAAGGGCGCG	CACACTGGCC
151	GGAAATTACCG	ACGGTTTCCG	TTTTTGGAC	AACGGGCGACG	ACATTTGCT
201	CGGCCCATAC	CGGGGGTGT	TGCCCCGTAT	GAAAACCATC	GGTTCAAGAC
251	CCCGTCCGC	CTTTTGCGC	GTACCGCTGC	ACTGGCATAT	GCACGGCGGT
301	TTGCAGTTCC	GCGCCCTCCC	CCTGCCCGCG	CCGCTGCATA	TTTGGGCGGG
351	CGTGTCTGCTT	GCCCCGGCGCG	TACCGTCCGC	ATTCAAAGCC	AAACTGCTTG
401	CCGATATGTC	CGATTGGCAG	AACTCCGCAC	GCCTCGGACA	GCCCGACACG
451	ACAGTTGCAC	AATGGCTGAA	ACAGCGGAAG	GTGCGCGCTG	CCGCCGTAAAT
501	GCAGTTTGG	CAGGCCCTTG	TCTGGGGCGC	GCTAACACG	CCTTTGGAAA
551	CCGCAAGCCT	GCGCGTGTG	TGCAACGTTT	TGTGCGACGG	CGTGTGCGAC
601	AAAAAAATCCG	GCAGCGACTA	TCTCCTACCC	AAACAGGATT	TGGGCGCAAT
651	CGTCGCCGAA	CCCGCCCTTG	CGGAGCTTCA	ACGGCTCGGC	GCGGACATCC
701	GCTCTGAAAC	GCGCGTATGC	CGTCTGAACA	CCCTCCCGGA	CGGAAAAGTC
751	CTCGTCAACG	GCGAAGCCTT	CGATGCCGCC	ATACTTGCCA	CCGGCGCCCTA
801	CCACGCCGCC	GCGCTCTCG	CGAAAGGCAC	GCCCGAACAC	GTTCAAGACG
851	CATATCAAAA	CCTTCGCTAC	CACGCCATCA	CCACCGTCTA	TCTGCGCTAC
901	GCCGAACCCG	TCCGcCTGcc	CGCCCCGCTG	AccGGCATtg	CCGAcggcAC
951	ggcaCaatgG	CTGCTTtgc	cgGGGGCAGGC	tccggactgc	CcccaaAacg
1001	aagTCTCCGC	cGTCAattgc	GTTCGGAcc	GGGtcggcgc	Gtttgc当地
	cga...				

This corresponds to the amino acid sequence <SEO ID 3014 ORF 997_ng>.

g997.pep (partial)

1 MMNTPHPRPK IAVIGAGWAG LSAAVTLARH ADVTLFEEAGR QAGGRARTLA
51 GNTDGFGLD NGOHILLGAY RGVLRLMKTI GSDFPRAAFLR VPLHWHMHGG
101 LQFRALPLPA PLHILGGVLL ARRVPASAFKA KLLADMSDLQ KSARLGQPDT
151 TVAQWLKQRN VPRAAVMQFW QPLVWGALNT PLETASLRVL CNVLSGDVLT
201 KKSGSDYLLP KQDLGAIVAE PALAELQRLG ADIRLETRVC RLNTLPDGKV
251 LVNGEAFDAA ILATAPYHAA ALLPEGTPEH VQTAYQNLRY HAITTVYLRY
301 AEPVRLPAPL TGIADGTAQW LLCPGQAPDC PQNEVSAVIS VSDRVGAFAN
351 R.....

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 3015>:

m997.seq

1	ATGATGAACA	CGCCGCATCC	GGCCTTGTAA	ATGCCCGTCA	TCCGGCGAGG
51	CTGGGCAGGA	CTGTCCGCCG	CCGTCACCTT	GGCGCGGCAC	GCCGACGTTA
101	CCCTGTTGAA	AGCCGGCCGG	CAGGCGGGCG	GCAGGGCGCG	CACACTGGCC
151	GGAAAATACCG	ACGGTTTCCG	TTTTTTGGAC	AACGGGCAGC	ACATTTTGCT
201	CGGGCCATAC	CGGGGGCTGT	TGGCCCTGTAT	GAAAACCATT	GTTCCGGATC
251	CCCCGTGCCGC	CTTTTTGGCC	GTACCGCTGC	ATGCGCATAT	GCACGGGGGT
301	TTGCAGTTCC	GCGCCCTCCC	CCTGCCCCGG	CCGCTGCATA	TTTTGGGGCGG
351	CCTGCTGCTT	GCCCCGGCTG	CACCGACTGC	ATTCAAAGCC	AAACTGCTT
401	CCGATATGTC	CGATTTGGCA	AAGTCCGCAC	GCCTCGGACA	GCCCCGACACG
451	ACAGTGGCGC	AATGGCTGAA	ACAGCGAAC	GTGCCGGCTG	CCGGCGTGTAT
501	GCAGTTTGGG	CAGCCCTTGG	TTTGGGGCGC	GCTCAACACG	TTTGGGGGAA

551	CCCGAAGCCT	GCGCGTGTG	TGCAACGTTT	TGTCCGAGCG	CGTGCTGACG
601	AAAAAAATCCG	GCAGCGACTA	TCTCCTACCC	AAGCAGGATT	TGGGCGCAAT
651	CCTCGCCGAA	CCCGCCTTGG	CGGATCTTC	ACGGCTCGGC	CGGGACATCC
701	GCCTCGAAC	GCGCTATGC	CGTCTGAACA	CCCTCCCGGA	CGGGAAAGTG
751	CTCTGCAACG	GCGAAGCTTT	CGATGCCGCC	GTCCCCGCCA	CGCGCCCTTA
801	CCACGCCGCC	GCGCTCTGC	CCGAAGGCAC	GCCCAGAACAC	GTTCAGACGG
851	CATATCAAAA	CCTTCGCTAC	CACGCCATCA	CCACCGTCTA	TCTGCGCTAC
901	GCCGAACCCG	TCCGCTCTGC	CGCCCCCGCT	ACGGCCCTTG	CCGACGGCAC
951	GGTGCATGG	CTGCTTGC	GGGGCAGGCT	CGGACTGCCT	GAAAACGAAG
1001	TGTCCGCGGT	CATCGCGGT	TCGACCGCG	TGCGCGCTT	TGCAAACCGG
1051	GGCGGGCGG	ACAAAGCCCA	CGCCGACCTC	AAACGCATCC	TTCCGATT
1101	GGGCGAACCC	GAAGCCGTGC	GCCTCATCAC	CGAAAACAGC	GCCACAACCG
1151	CAGCCGATGC	CCCGCCGCCG	GACTTGTCTG	GGTTGCAACCG	GCACCGCATC
1201	TTCCCCGCCG	GCGACTACCT	CCACCCGGAC	TACCCCGCCA	CGCTCGAAGC
1251	CGCGGTACAA	TCAGGTTTCG	CGTCGGCGGA	AGCCTGCCTG	CAAAGCCTGA
1301	GGCATGCCGT	CTGA			

This corresponds to the amino acid sequence <SEQ ID 3016; ORF 997>;

m997.pep

1 MMNTPHPRPK IAVIGAGWAG LSAAVTLARH ADVTLEFAGR QAGGRARTLA
51 GNTDGFGLND NGOHILLGAY RGVLRLMKTI GSDPRAAFLR VPLHWHMHGG
101 LQFRALPLPA PLHILGGVL ARRAPTAFKA KLLADMSDLQ KSARLGQPDT
151 TVAQWLKQRN VPRAAVMQFWQ QPLVWGAINT PLETASLRLV CNVLSDGVL
201 KKSGSDYLLP KQDLGAIVAE PALADLQLRG ADIRLETRVC RINTLPDGKV
251 LVNGEAFDAA VPATAPYHAA ALLPEGTPEH VQTAYQNLRY HAITTVYLRY
301 AEPVRLPAPL TGLADGTQVWQ LLCRGRGLGP ENEVSASIVS SDRVGAFANR
351 AWADAKAHAD KLRLPHLGEP EAERVITEKRR ATTAADAPP DLSWLHRHRI
401 FPAGDYLHPD YPATLEAAVQ SGFASAEACL QSLSDAV*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 997 shows 96.0% identity over a 351 aa overlap with a predicted ORF (ORF 997) from *N. gonorrhoeae*

g997/m997 96.0% identity in 351 aa overlap

	10	20	30	40	50	60
g997.pep	MMNTPHPRKIAVIGAGWAGLSAAVTLARHADVTLFEAGRQAGGRARTLAGNTDGFGLD					
m997	MMNTPHPRKIAVIGAGWAGLSAAVTLARHADVTLFEAGRQAGGRARTLAGNTDGFGLD					
	10	20	30	40	50	60
g997.pep	70	80	90	100	110	120
m997	NGQHILLGAYRGVLRLMKTIGSDPRAAFLRVPLHWHMHGGLQFRALPLPAPLHILGGVLL					
g997.pep	70	80	90	100	110	120
m997	NGQHILLGAYRGVLRLMKTIGSDPRAAFLRVPLHWHMHGGLQFRALPLPAPLHILGGVLL					
	130	140	150	160	170	180
g997.pep	ARRVPSAFKAKLLADMSDLQKSARLGQPDTTVAQWLKQRNVPRAAVMQFWQPLVWGALNT					
m997	ARRAPTAFKAKLLADMSDLQKSARLGQPDTTVAQWLKQRNVPRAAVMQFWQPLVWGALNT					
g997.pep	130	140	150	160	170	180
m997						
	190	200	210	220	230	240
g997.pep	PLETASLRVLCNVLSDGVLTGKSGSDYLLPKQDLGAIVAEPALAEQLRLGADIRLETRVC					
m997	PLETASLRVLCNVLSDGVLTGKSGSDYLLPKQDLGAIVAEPALADLRLGADIRLETRVC					
g997.pep	190	200	210	220	230	240
m997						
	250	260	270	280	290	300
g997.pep	RLNTLPDGKVLVNGEAFDAAILATAPYHAALLPEGTPEHVQTAYQNLRYHAITTVYLRY					
m997	RLNTLPDGKVLVNGEAFDAAVPATAPYHAALLPEGTPEHVQTAYQNLRYHAITTVYLRY					
g997.pep	250	260	270	280	290	300
m997						
	310	320	330	340	350	
g997.pep	AEPVRLPAPLTGIADGTAQWLICPGQAPDCPQNNEVSAVISVSDRVGAFANR					
m997	AEPVRLPAPLTGLADGTVOWLICRGRL-GLPENEVSAVISVSDRVGAFANRAWADKAHD					
g997.pep	310	320	330	340	350	
m997						

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3017>:

a997.seq

```

1 ATGATGAACA CGCCGCATCC GCGCCCGAAA ATCGCCGTCA TCGGCGCAGG
51 CTGGGCCGGC TTGTCCGCCG CCCTTACCTT GCGCGGGCAC GCGGACGTTA
101 CCCGTGTTGA AGCCGCCGG CAGGCCGGCG GCAGGGCGCG CGCACTGGCC
151 GGAAATACCG ACGGTTTCGG TTTTTGGAC AACGGGCAGC ATATTTACT
201 CGGCGCATAC CGGGCGCTGT TGCCGCTGAT GAAAACCATC GGTCAGACC
251 CCCATGCCGC CTTTTGCGC GTACCGCTGC ACTGGCATAT GCACGGCGGT
301 TTGCAGTTGC GCGCCCTCCC CCTGGCCGATA CCCCTGCATA TTTTGGCGG
351 CGTGCTGCTT GCGCCGGCGC TACCGTCCGC ATTCAAAGCC AAACGTGTTG
401 CGCATATGTC CGATTGCAAG AAGTCCGCAC GCCTCGGACA GCCCGACACG
451 ACAGTGGCGC AATGGCTGAA ACAGCGGAAC GTGCCGCGTG CCGCCGTAAT
501 GCAGTTTGG CAGGCCCTGG TTTGGGGCGC GCTCAACACG CCTTTGGAAA
551 CGCGAAGCGC CGCGCTGTT TGCAACGTT TGTCGGACGG CGTGCTGACG
601 AAAAACATCCG GCAGCGACTA TCTCCCTACCC AAACAGGATT TGGGCGCAAT
651 CGTCGCCGAA CCCGCCCTGG CGGAGCTTC ACGGCTCGGC CGGGACATCC
701 GCCTCGAAAC GCGCATATGC CGTCTGAACA CCCTCCCGGA CGGGAAAGTG
751 CTCGTCAACG GCGAAACCTT CGATGCCGCC GTCCCCGCCA CGCGCCCTA
801 CCACGCCGCCGCGCCTGC CGCAAGGCCAC GCGCGAACAC GTTCAGACGG
851 CATATCAAAA CCTCGCTAT CACGCCATCA CCACCGTCTA TCTGCGCTAT
901 GCCGAACCCG TCCGCTTGCC TGCCCCCTG ACCGGACTTG CCGACGGCAC
951 GGTGCAATGG CTGCTTGCC GGGCGAGGCT CGGACTGCT GAAAACGAAG
1001 TGTCCGCGGT CATCGCGTT TCCGACCGCG TCAGCGCGTT TGCAAACCGG
1051 GCGTGGGGCGG ACAAAAGTTCA CGCCGACCTC AAACGCACTT TTCCGCATT
1101 GGGCGAACCC GAAGCGCTGC GCGTCATCAC CGAAAAACGC GCCACAACCG
1151 CAGCCGATGC CCCGCCGCCG GATTGCTGTT GGTTGACCG GCACCGCATC
1201 TTCCCCGCCG GCGACTACCT CCACCCAGAC TACCCGCCA CGCTCGAAGC
1251 CGCGTACAA TCAGGTTTCG CGTCGGCGGA AGCCTGCTG CAAAGCCTGA
1301 CGCGATGCCGT CTGA

```

This corresponds to the amino acid sequence <SEQ ID 3018; ORF 997.a>:

a997.pep

```

1 MMNTPHPRK IAVIGAGWAG LSAAVTLARH ADVTLFTEGR QAGGRARALA
51 GNTDGFGLD NGQHILLGAY RGVLRLMKTI GSDPHAAFLR VPLWHMHMG
101 LQFRALPLPA PLHILGGVLL ARRVPSAFKA KLLADMSDLQ KSARLGQPDT
151 TVAQWLKQRN VPRAAVMQFW QPLVWGAINT PLETASLRVL CNVLSDGVL
201 KKSGSDYLLPK QDLAGIAVAE PALAEQLRLG ADIRLETRIC RLNTLPDGKV
251 LVNGEPFDAA VPATAPYHAA ALLPEGTPEH VQTAYQNLRY HAITTVYLRY
301 AEPVRLPAPL TGLADGTQW LLCRGRGLGP ENEVSAVISV SDRVGAFAWR
351 AWADKVHADL KRILPHLGEV EAVRVITEKR ATTAADAPP DLSWLHRHRI
401 FPAGDYLHPD YPATLEAAVQ SGFASAEACL QSLDAV*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 997 shows 98.2% identity over a 437 aa overlap with a predicted ORF (ORF 997) from *N. meningitidis*

a997/m997 98.2% identity in 437 aa overlap

a997.pep	10	20	30	40	50	60
	MMNTPHPRKIAVIGAGWAGLSAAVTLARHADVTLFTEGRQAGGRARALAGNTDGFGLD					
m997	10	20	30	40	50	60
	MMNTPHPRKIAVIGAGWAGLSAAVTLARHADVTLFTEGRQAGGRARTLAGNTDGFGLD					
a997.pep	70	80	90	100	110	120
	NGQHILLGAYRGVLRLMKTIGSDPHAAFLRVPLHWHMHGGLQFRALPLPAPLHILGGVLL					
m997	70	80	90	100	110	120
	NGQHILLGAYRGVLRLMKTIGSDPRAAFLRVPLHWHMHGGLQFRALPLPAPLHILGGVLL					
a997.pep	130	140	150	160	170	180
	ARRVPSAFKAKLLADMSDLQKSARLGQPDTTVAOWLKQRNVPRAAVMQFWQPLVWGAINT					
m997	130	140	150	160	170	180
	ARRAPTAFKAKLLADMSDLQKSARLGQPDTTVAOWLKQRNVPRAAVMQFWQPLVWGAINT					
a997.pep	190	200	210	220	230	240
	PLETASLRVLCNVLSDGVLTKKGSDYLLPKQDLGAIAVAEPALAEQLRLGADIRLETRIC					

1419

m997	PLETASLRVLCNVLSGVLTKSGSDYLLPKQDLGAIVAEPALADLQLRGADIRLETRVC					
	190	200	210	220	230	240
a997.pep	250	260	270	280	290	300
	RLNTLPDGKVLVNGEPEPFDAAVPATAPYHAAALLPEGTPHEHVQTAYQNLRYHAITTVYLRY					
m997	RLNTLPDGKVLVNGEAFDAAVPATAPYHAAALLPEGTPHEHVQTAYQNLRYHAITTVYLRY					
	250	260	270	280	290	300
a997.pep	310	320	330	340	350	360
	AEPVRLPAPLTGLADGTVQWLICRGRGLPENEVSAVISVSDRVGAFAWRADKVHADL					
m997	AEPVRLPAPLTGLADGTVQWLICRGRGLPENEVSAVISVSDRVGAFAWRADKAHADL					
	310	320	330	340	350	360
a997.pep	370	380	390	400	410	420
	KRILPHLGEPEAVRVITEKRATTAADAPPDLSWLHRHRIFPAGDYLHPDYPATLEAAVQ					
m997	KRILPHLGEPEAVRVITEKRATTAADAPPDLSWLHRHRIFPAGDYLHPDYPATLEAAVQ					
	370	380	390	400	410	420
a997.pep	430 SGFASAEACLQSLSDAVX					
m997	SGFASAEACLQSLSDAVX					
	430					

g999.seq Not found yet**g999.pep Not found yet**The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3019>:**m999.seq**

```

1 ATGAATATGA AAAAATTGAT TTCCGCAATT TGTGTTCAA TTGTTTATC
51 AGCCTGCAAC CAACAATCAA AAACGGCACA ACCCGAAGAA CCTGTCCAAA
101 GTATCCAGGC TGCTGATTGT ACCGCCCAA TGGACATCAC AGTTGAACAA
151 TATCTCATCA ATTTGGAGCA AGCATTTAAA ACTCAGAACG TCTCAACAAA
201 AATCCATAAT AAAAATATTG TCAAGACCGA TTGTGGTTAT GACCTTACTT
251 TGGTAATGGA TTTTGGGGCG ATTGCGCTCA AACTGGACGA GCAGCAAAAA
301 ATTAGAGCTA TCTCACTAGG CTACATTTTA AAAACCGACG GAGAGAAAGG
351 ACAAAATCTA GTCAATAATG CCATAAAATGG ATTACACAGT ATTCAAGGCAG
401 TTCTGTCTT AACTACCACA GACAAATTGG CGAATCGGA AGCAGGAAAA
451 CAACTTTTA CAGCTTTAAC CGAAGTCGTC AAAGAATCCA ATCAGACAGG
501 AGCAACAGCG CAAAAAGACG TTCCGGCAGA TGGTATTTA TATAGCGTTG
551 TTTTGAAAA AGAAACAAAC ACCATTGCAA TAATCGGCAG AAAACAACCC
601 TAA

```

This corresponds to the amino acid sequence <SEQ ID 3020; ORF 999>:

m999.pep

```

1 MNMKKLISAI CVSIVL SACN QQS KTAQAEF PVQ SIQAADC TAPMDITVEQ
51 YLIN LEQAFK TQN VSTKIH KNIV KTDCGY DLT LVMDFGA IALKLDEQQK
101 IRA ISVG YIL KTD GEKG QNL VNN AIINGLHS IQAVL SLT TT DKL GESEAGK
151 QLFT ALTEVV KES NQTGATA QKD VPADGIL YSV VF EKETN TIAI IGRKQP
*

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a999.seq Not found yet**a999.pep Not found yet**

The foregoing examples are intended to illustrate but not to limit the invention.

CLAIMS

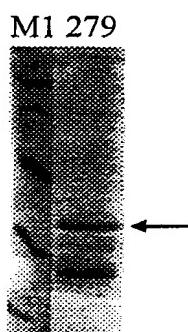
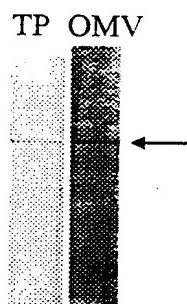
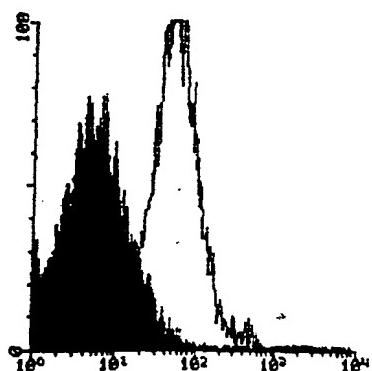
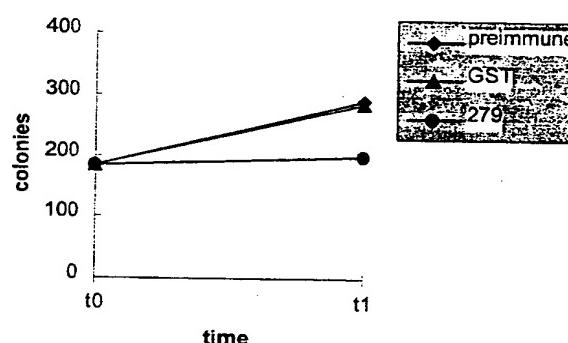
1. A protein comprising a fragment of an amino acid sequence from SEQ ID 2790 wherein said fragment comprises at least 7 amino acids from said sequence.
2. A protein comprising an amino acid sequence selected from the group consisting of even numbered SEQ IDs from SEQ ID number 2 through SEQ ID number 3020.
3. A protein having 50% or greater homology to a protein according to claim 1.
4. A protein comprising a fragment of an amino acid sequence selected from the group consisting of even numbered SEQ IDs from SEQ ID number 2 through SEQ ID number 3020, wherein said fragment comprises 7 or more consecutive amino acids from said sequence.
5. An antibody which binds to a protein according to any one of claims 1 to 3.
6. A nucleic acid molecule which encodes a protein according to any one of claims 1 to 3.
7. A nucleic acid molecule according to claim 5, comprising a nucleotide sequence selected from the group consisting of odd numbered SEQ IDs from SEQ ID number 1 through SEQ ID number 3019.
8. A nucleic acid molecule comprising a fragment of a nucleotide sequence selected from the group consisting of odd numbered SEQ IDs from SEQ ID number 1 through SEQ ID number 3019, wherein said fragment comprises 10 or more consecutive nucleotides from said sequence.
9. A nucleic acid molecule comprising a nucleotide sequence complementary to a nucleic acid molecule according to claim 5.
10. A nucleic acid molecule comprising a nucleotide sequence complementary to a nucleic acid molecule according to claim 6.
11. A nucleic acid molecule comprising a nucleotide sequence complementary to a nucleic acid molecule according to claim 7.
12. A composition comprising a protein, a nucleic acid molecule, or an antibody according to any preceding claim.
13. A composition according to claim 11 being a vaccine composition or a diagnostic composition.
14. A composition according to claim 11 for use as a pharmaceutical.
15. The use of a composition according to claim 11 in the manufacture of a medicament for the treatment or prevention of infection due to Neisserial bacteria.

1421

16. A composition comprising a protein of claim 1 wherein said composition is immunogenic.

17. A composition comprising a protein of claim 2 wherein said composition is immunogenic.

18. A composition comprising a protein of claim 3 wherein said composition is immunogenic.

279 (10.5 kDa)**Fig. 2****A) PURIFICATION****B) WESTERN BLOTH****C) FACS****D) BACTERICIDAL ASSAY****E) ELISA assay: positive****279**

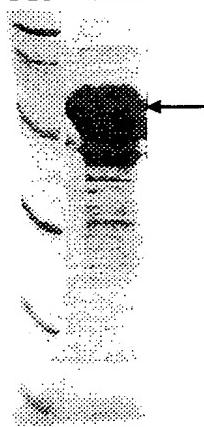
The predicted gene 279 was cloned in pGex vector and expressed in *E. coli*. The product of protein expression and purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 279-GST purification. Mice were immunized with the purified 279-GST and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that protein 279 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

576 (27.8 kDa)

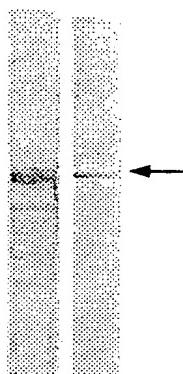
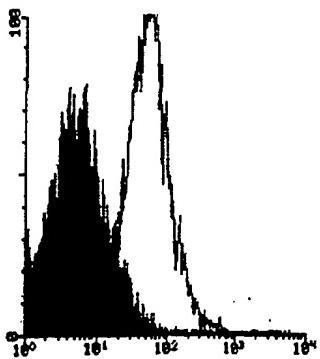
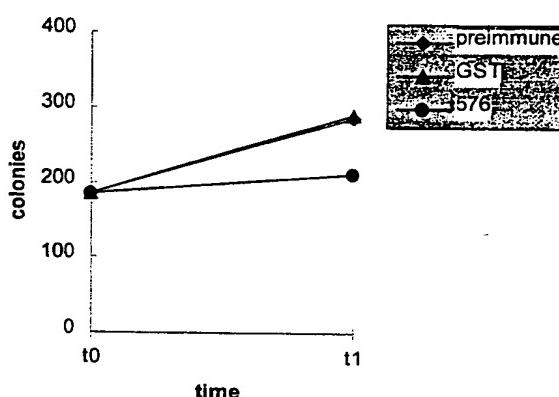
Fig. 3

A) PURIFICATION

M1 576

**B) WESTERN BLOT**

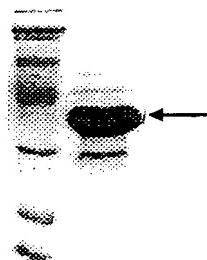
TP OMV

**C) FACS****D) BACTERICIDAL ASSAY****E) ELISA assay: positive****576**

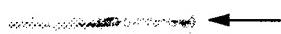
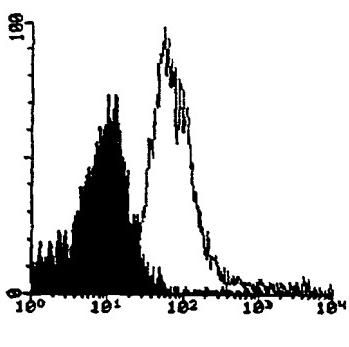
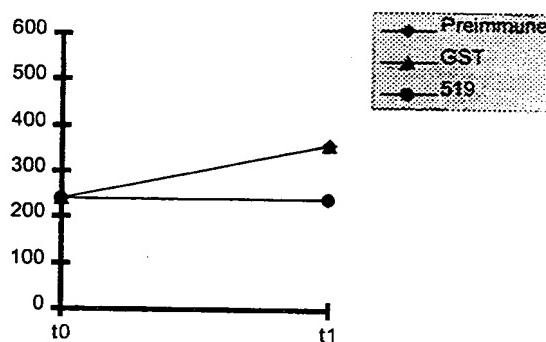
The predicted gene 576 was cloned in pGex vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 576-GST fusion protein purification. Mice were immunized with the purified 576-GST and sera were used for Western blot (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that 576 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

519 (33 kDa)**Fig. 4****A) PURIFICATION**

M1 519

**B) WESTERN BLOTH**

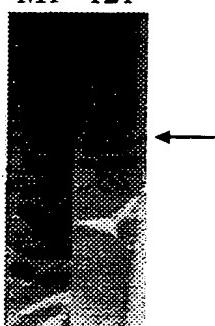
TP OMV

**C) FACS****D) BACTERICIDAL ASSAY****E) ELISA assay: positive****519**

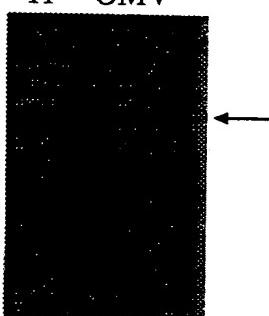
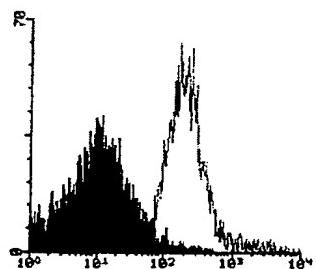
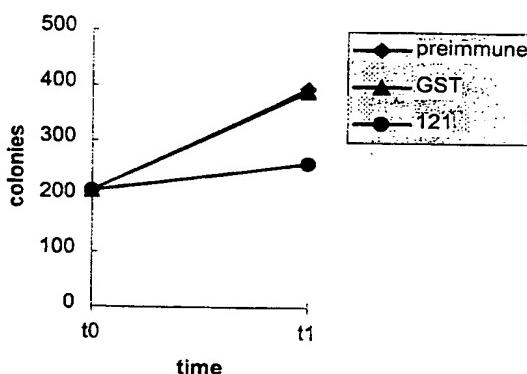
The predicted gene *519* was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 519-His fusion protein purification. Mice were immunized with the purified 519-His and sera were used for Western blot (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that 519 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

121 (40 kDa)**A) PURIFICATION**

M1 121

**B) WESTERN BLOTH**

TP OMV

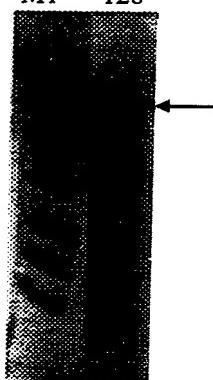
**C) FACS****D) BACTERICIDAL ASSAY****E) ELISA assay: positive****121**

The predicted gene *121* was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 121-His fusion protein purification. Mice were immunized with the purified 121-His and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that 121 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

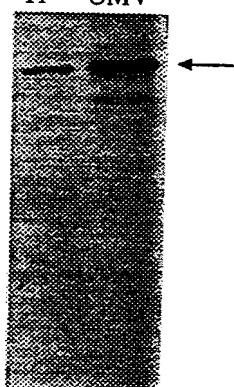
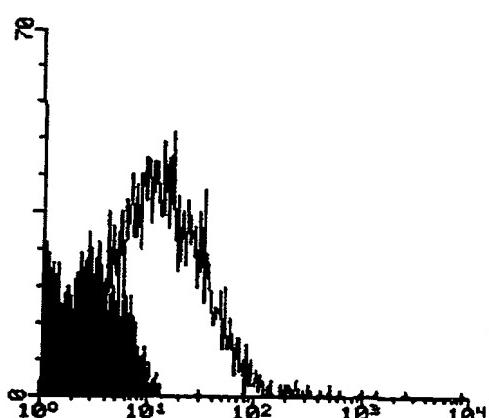
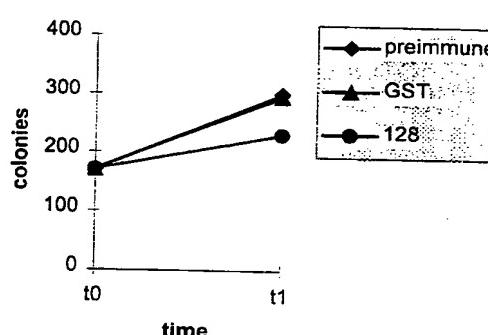
Fig. 5

128 (101 kDa)**Fig. 6****A) PURIFICATION**

M1 128

**B) WESTERN BLOTH**

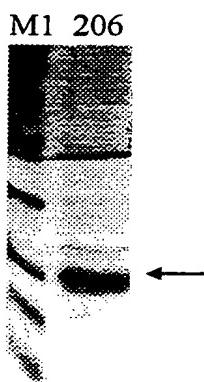
TP OMV

**C) FACS****D) BACTERICIDAL ASSAY****E) ELISA assay: positive****128**

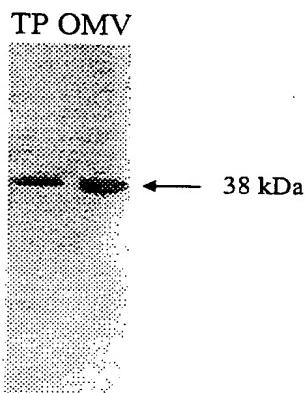
The predicted gene *128* was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 128-His purification. Mice were immunized with the purified 128-His and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D) and ELISA assay (panel E). Results show that 128 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

Fig. 7

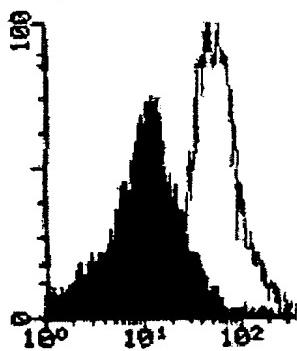
A) PURIFICATION



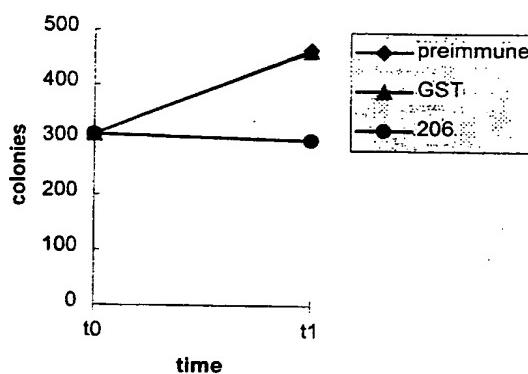
B) WESTERN BLOTH



C) FACS



D) BACTERICIDAL ASSAY



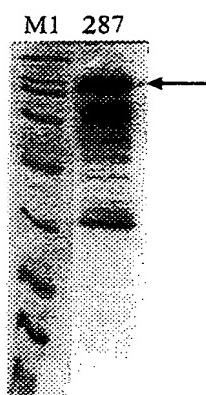
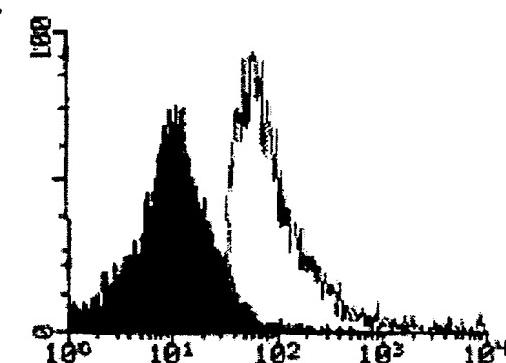
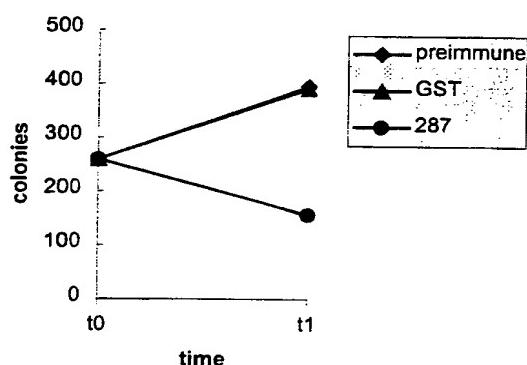
E) ELISA assay: positive

206

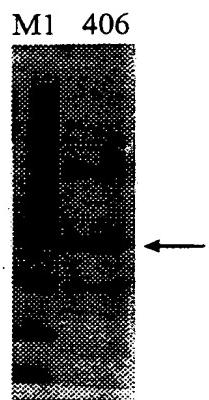
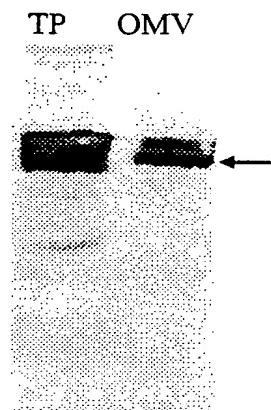
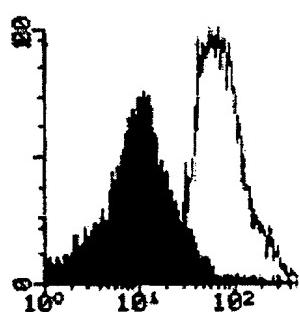
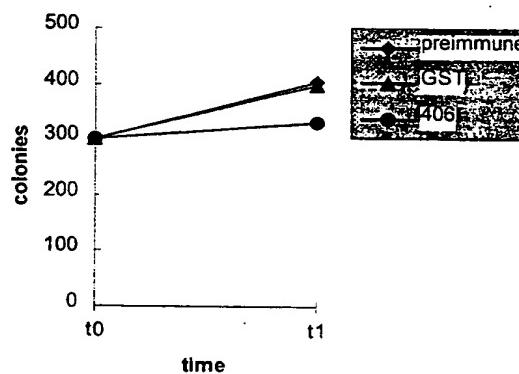
The predicted gene 206 was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 206-His purification. Mice were immunized with the purified 206-His and sera were used for Western blot analysis (panel B). It is worthnoting that the immunoreactive band in protein extracts from meningococcus is 38 kDa instead of 17 kDa (panel A). To gain information on the nature of this antibody staining we expressed ORF 206 in *E. coli* without the His-tag and including the predicted leader peptide. Western blot analysis on total protein extracts from *E. coli* expressing this native form of the 206 protein showed a recative band at a position of 38 kDa, as observed in meningococcus. We conclude that the 38 kDa band in panel B) is specific and that anti-206 antibodies, likely recognize a multimeric protein complex. In panel C is shown the FACS analysis, in panel D the bactericidal assay, and in panel E) the ELISA assay. Results show that 206 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

287 (78 kDa)

Fig. 8

A) PURIFICATION**B) FACS****C) BACTERICIDAL ASSAY****D) ELISA assay : positive****287**

The predicted gene 287 was cloned in pGex vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 287-GST fusion protein purification. Mice were immunized with the purified 287-GST and sera were used for FACS analysis (panel B), bactericidal assay (panel C), and ELISA assay (panel D). Results show that 287 is a surface-exposed protein. Symbols: M1, molecular weight marker. Arrow indicates the position of the main recombinant protein product (A).

406 (33 kDa)**Fig. 9****A) PURIFICATION****B) WESTERN BLOTH****C) FACS****D) BACTERICIDAL ASSAY****E) ELISA assay : positive****406**

The predicted gene 406 was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 406-His fusion protein purification. Mice were immunized with the purified 406-His and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that 406 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

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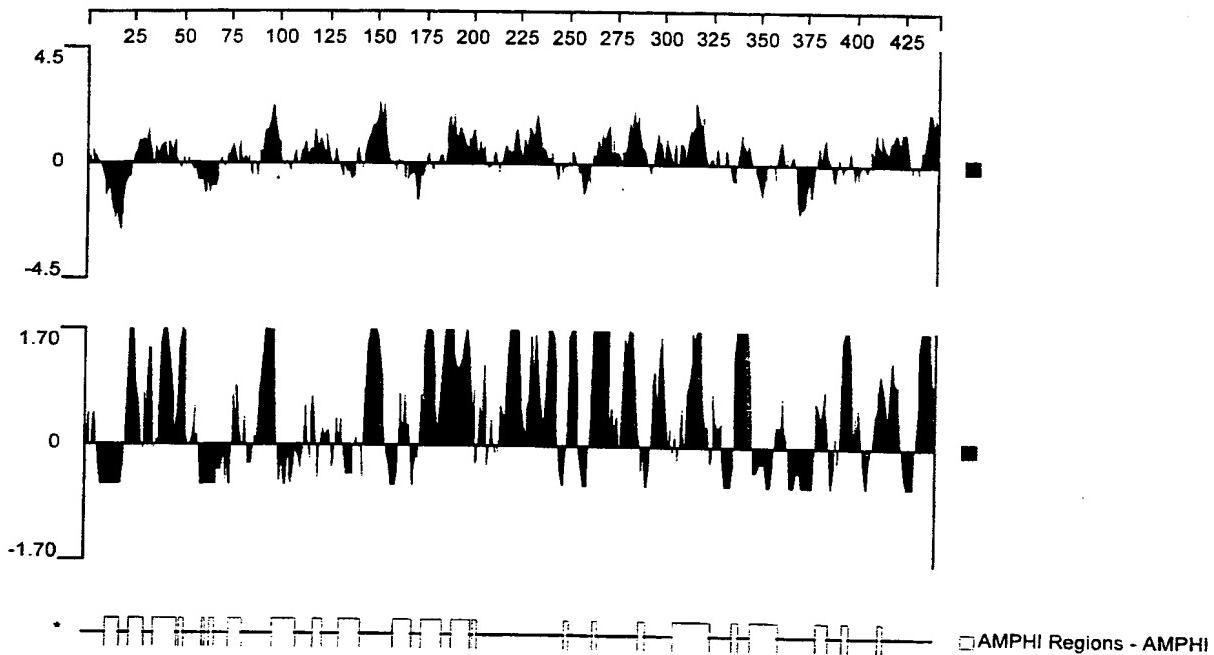
919Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 10

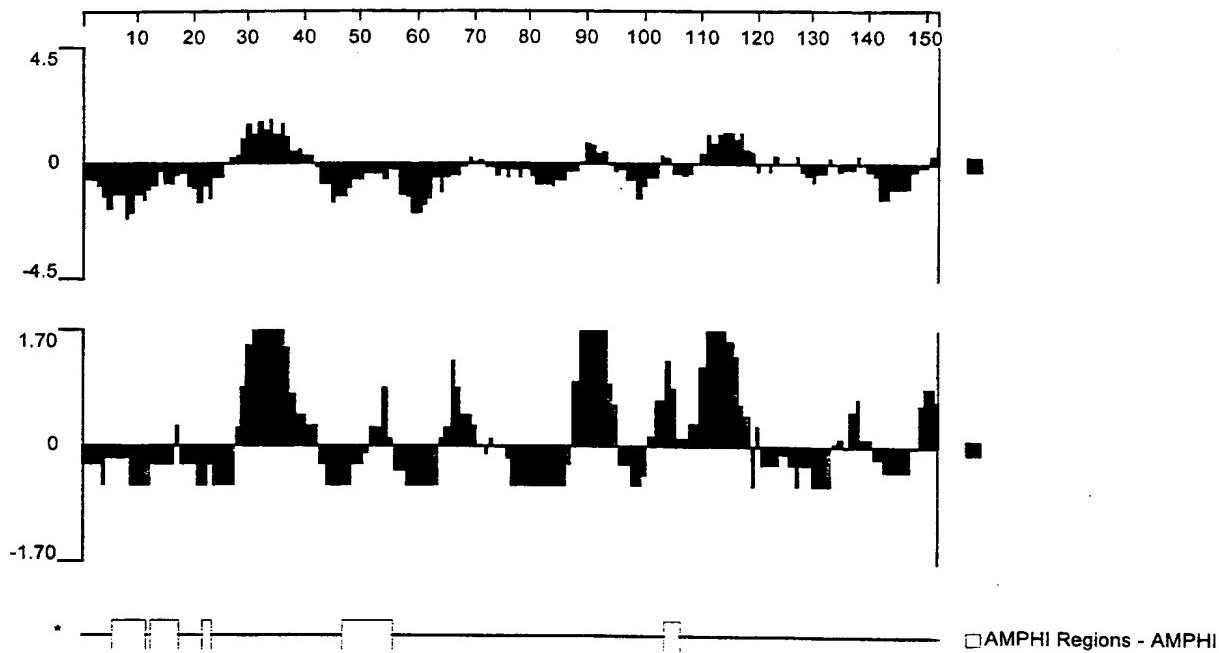
Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 11

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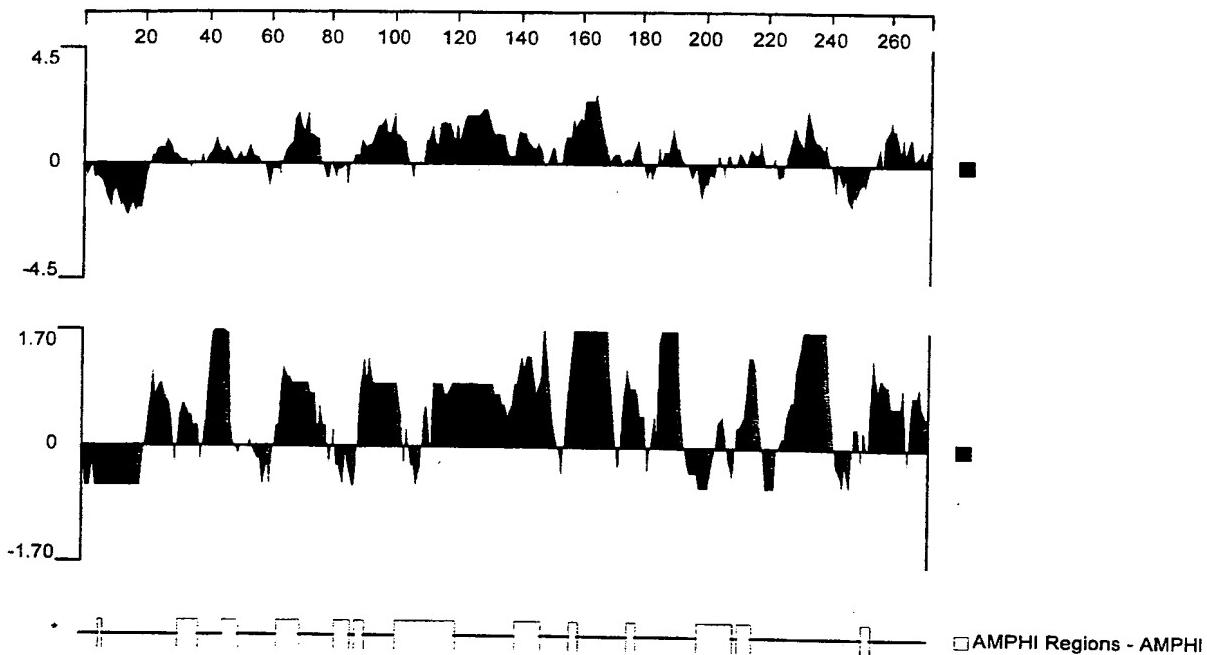
576-1Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 12

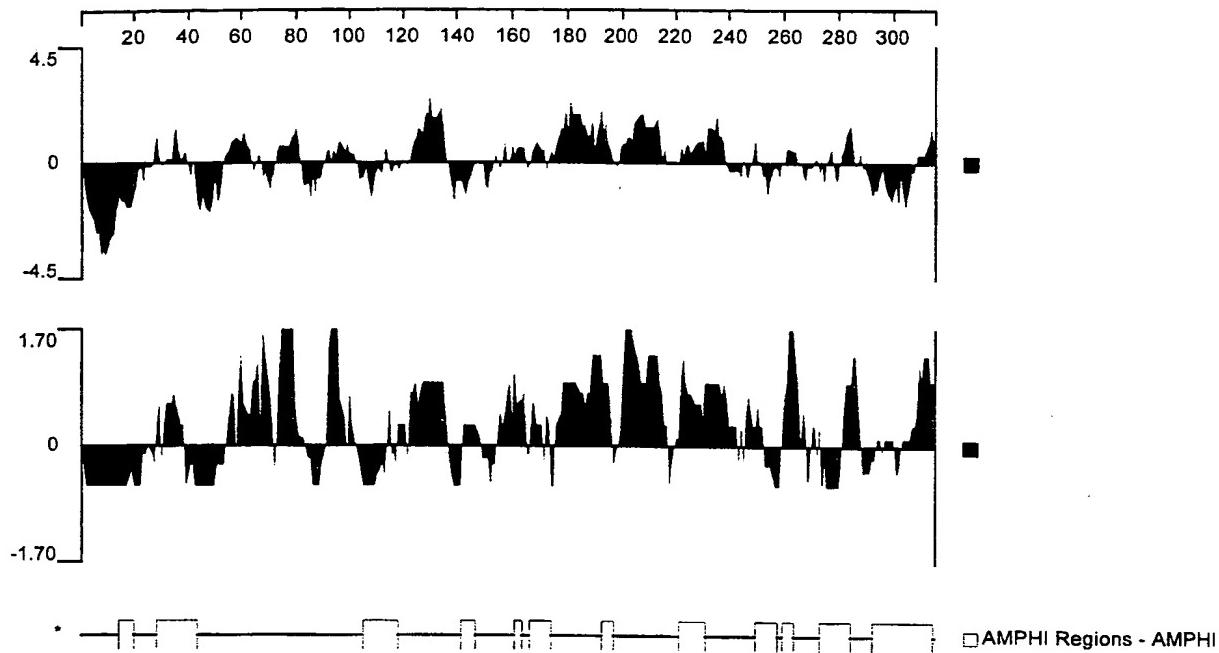
519-1Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 13

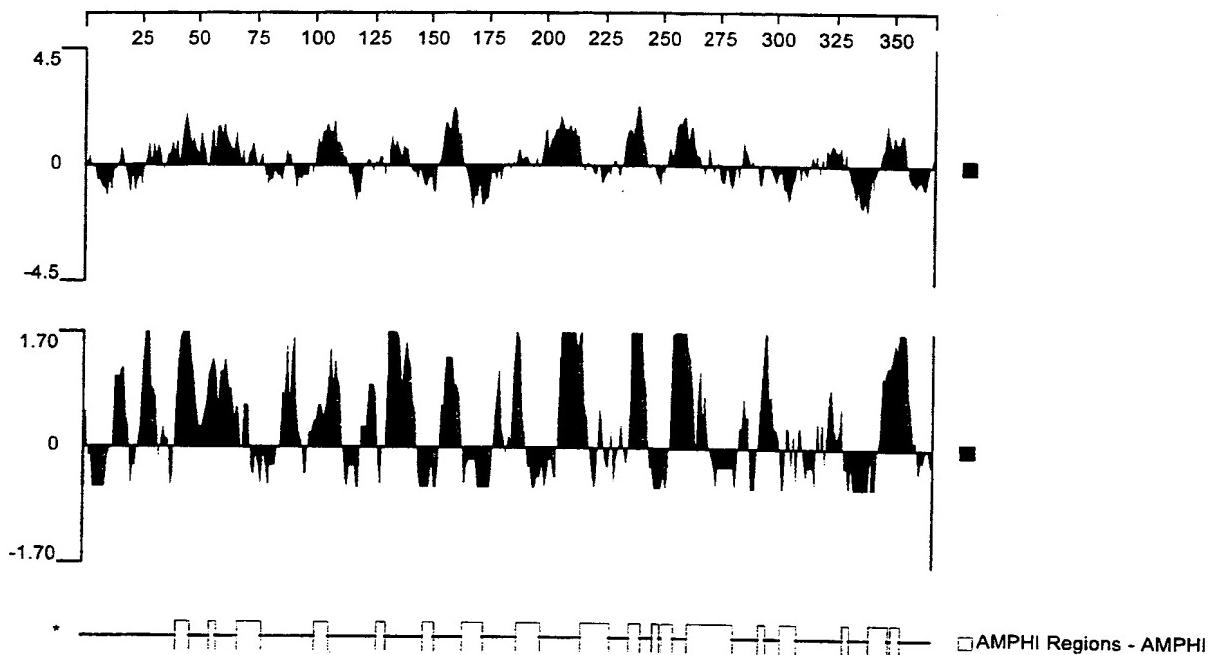
121-1Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 14

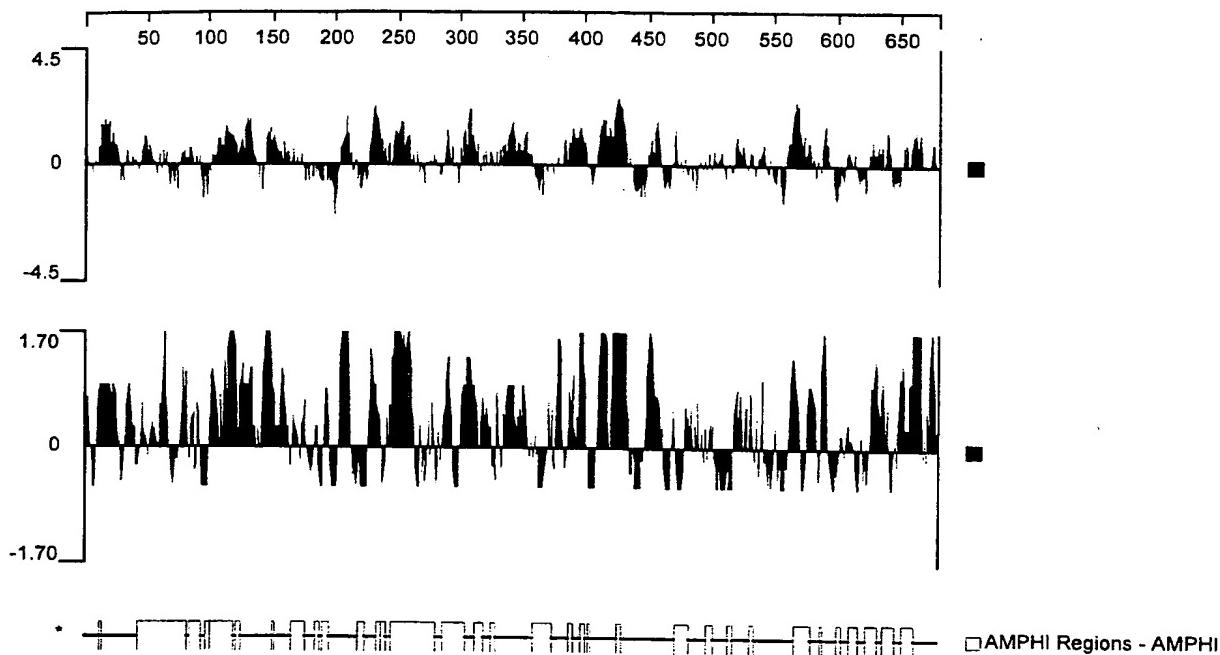
128-1Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 15

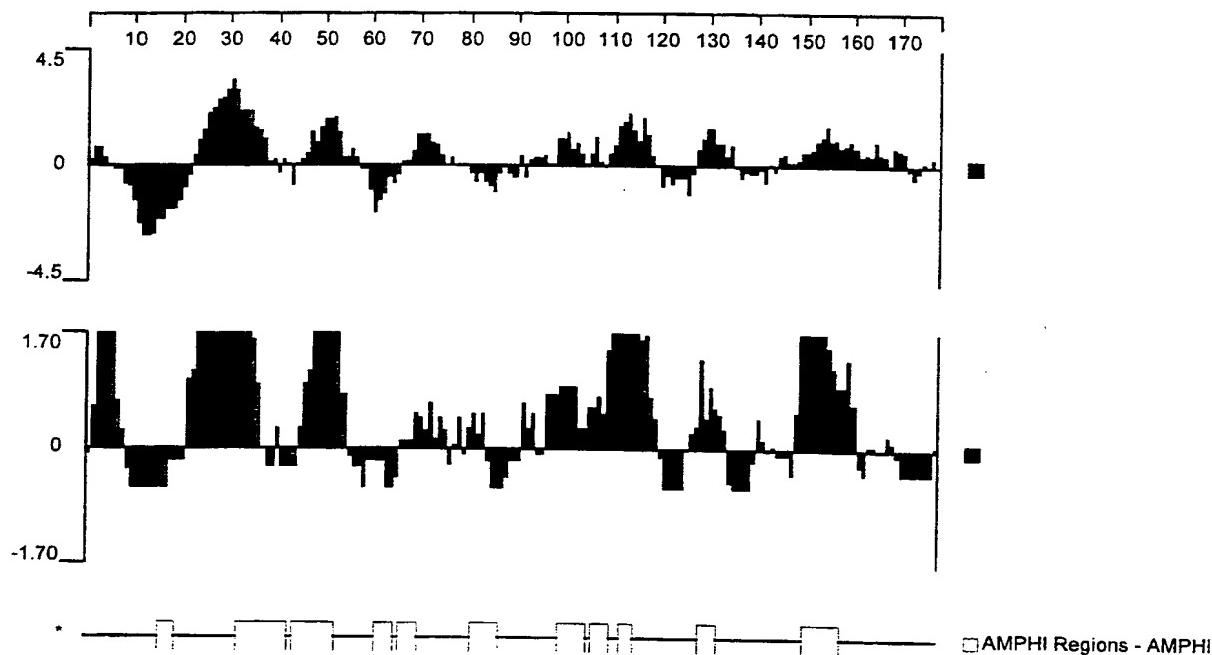
Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 16

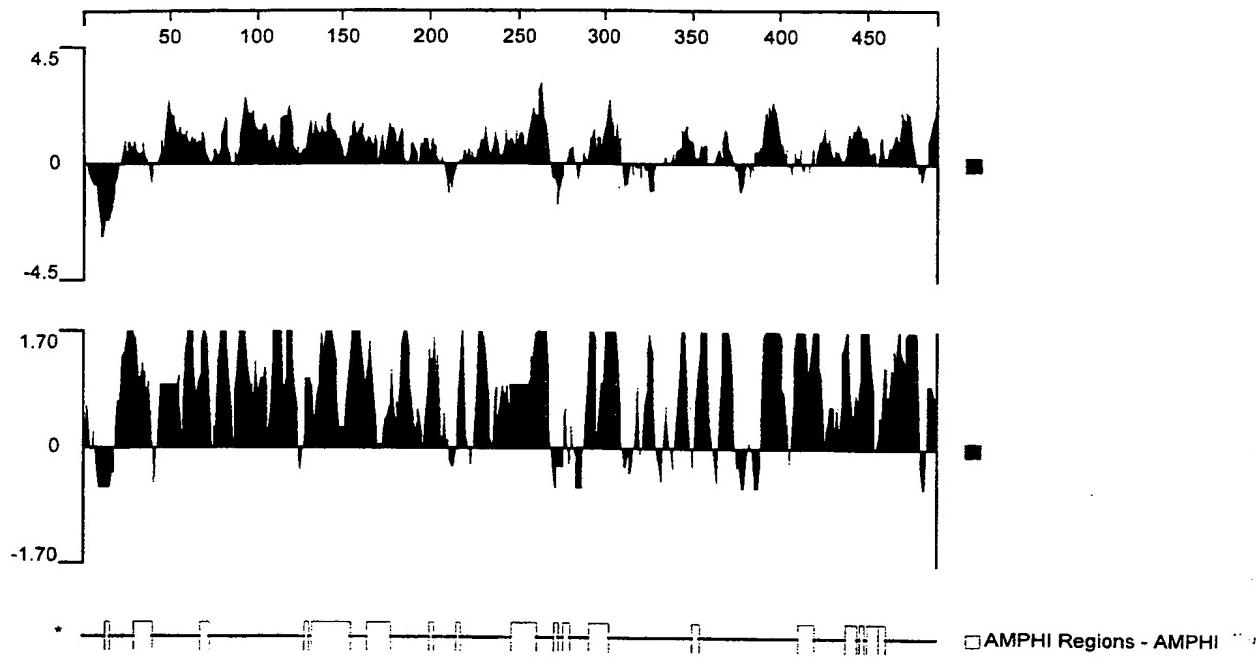
287Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 17

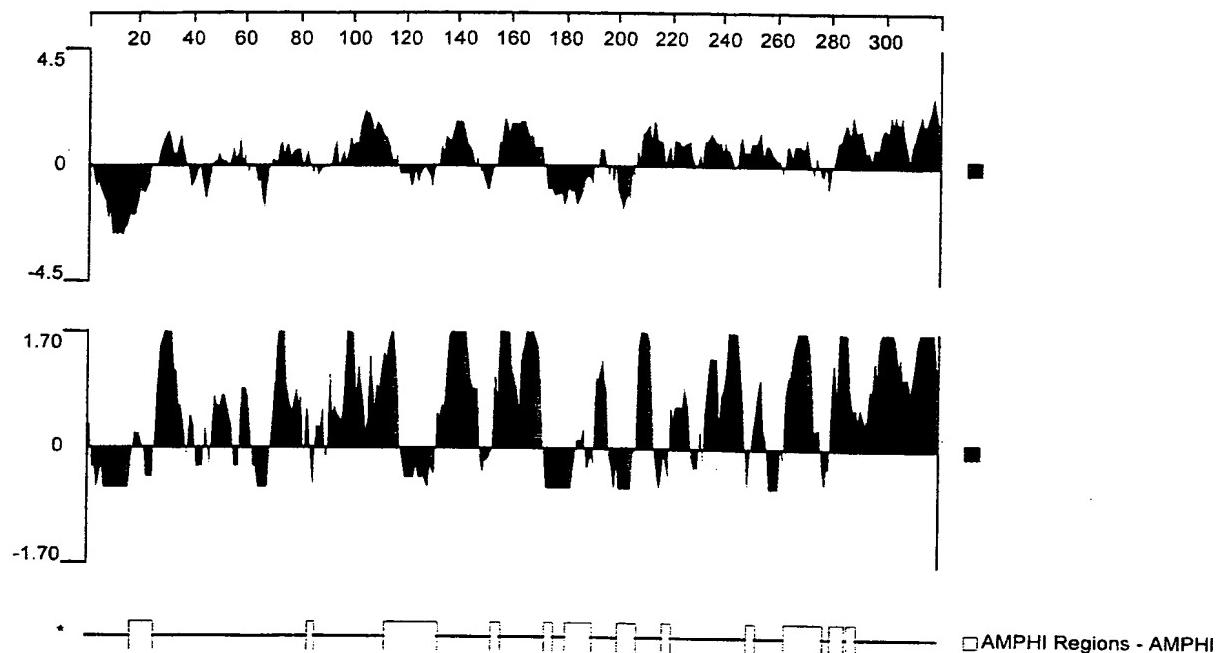
406Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 18

zo05_225	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLSSREQILRQFAEDEQPVLPINRAPARRAG		
zo08_225	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLSSREQILRQFAEDEQPVLPINRAPARRAG		
z2491	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLSSREQILRQFAEDEQPVLPINRAPARRAG		
zo11_225	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLSSREQILRQFAEDEQPVLPINRAPARRAG		
zo20_225	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLSSREQILRQFAEDEQPVLPINRAPARRAG		
zo01_225	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLSSREQILRQFAEDEQPVLPINRAPARRAG		
zo09_225	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLSSREQILRQFAEDEQPVLPINRAPARRAG		
zo12_225	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLSSREQILRQFAEDEQPVLPINRAPARRAG		
zo22_225	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLSSREQILRQFAEDEQPVLPINRAPARRAG		
zo23_225	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLSSREQILRQFAEDEQPVLPINRAPARRAG		
zo24_225	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLSSREQILRQFAEDEQPVLPINRAPARRAG		
zo25_225	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLSSREQILRQFAEDEQPVLPINRAPARRAG		
zo26_225	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLSSREQILRQFAEDEQPVLPINRAPARRAG		
zo96_225	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLSSREQILRQFAEDEQPVLPINRAPARRAG		
zo02_225	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLSSREQILRQFAEDEQPVLPINRAPARRAG		
zo04_225	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLSSREQILRQFAEDEQPVLPINRAPARRAG		
zo06_225	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLSSREQILRQFAEDEQPVLPINRAPARRAG		
zo07_225	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLSSREQILRQFAEDEQPVLPINRAPARRAG		
zo10_225	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLSSREQILRQFAEDEQPVLPINRAPARRAG		
zo14_225	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLSSREQILRQFAEDEQPVLPINRAPARRAG		
zo16_225	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLSSREQILRQFAEDEQPVLPINRAPARRAG		
zo17_225	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLSSREQILRQFAEDEQPVLPINRAPARRAG		
zo18_225	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLSSREQILRQFAEDEQPVLPINRAPARRAG		
zo19_225	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLSSREQILRQFAEDEQPVLPINRAPARRAG		
zo21_225	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLSSREQILRQFAEDEQPVLPINRAPARRAG		
zo27_225	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLSSREQILRQFAEDEQPVLPINRAPARRAG		
zo28_225	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLSSREQILRQFAEDEQPVLPINRAPARRAG		
zo29_225	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLSSREQILRQFAEDEQPVLPINRAPARRAG		
zo13_225	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLSSREQILRQFAEDEQPVLPINRAPARRAG		
zo03_225	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLSSREQILRQFAEDEQPVLPINRAPARRAG		
zo15_225	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLSSREQILRQFAEDEQPVLPINRAPARRAG		
fa1090	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLSSREQILRQFAEDEQPVLPINRAPARRAG		
zo32_225	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLSSREQILRQFAEDEQPVLPINRAPARRAG		
zo33_225	1	MDSFFKPAVWAVLWLMFAVRPALADELTNLSSREQILRQFAEDEQPVLPINRAPARRAG		
zo05_225	61	NADELIGSAMGLNE	QPVLPVNRVPARRAGNA
zo08_225	61	NADELIGSAMGLNE	QPVLPVNRVPARRAGNA
z2491	61	NADELIGSAMGLNE	QPVLPVNRVPARRAGNA	QPVLPVNRVPARRAGNA
zo11_225	61	NADELIGSAMGLNE	QPVLPVNRVPARRAGNA	QPVLPVNRVPARRAGNA
zo20_225	61	NADELIGSAMGLNE	QPVLPVNRVPARRAGNA	QPVLPVNRVPARRAGNA
zo01_225	61	NADELIGSAMGLNE	QPVLPVNRVPARRAGNA	QPVLPVNRVPARRAGNA
zo09_225	61	NADELIGSAMGLNE	QPVLPVNRVPARRAGNA
zo12_225	61	NADELIGSAMGLNE	QPVLPVNRVPARRAGNA
zo22_225	61	NADELIGSAMGLNE	QPVLPVNRVPARRAGNA
zo23_225	61	NADELIGSAMGLNE	QPVLPVNRVPARRAGNA
zo24_225	61	NADELIGSAMGLNE	QPVLPVNRVPARRAGNA
zo25_225	61	NADELIGSAMGLNE	QPVLPVNRVPARRAGNA
zo26_225	61	NADELIGSAMGLNE	QPVLPVNRVPARRAGNA
zo96_225	61	NADELIGSAMGLNE	QPVLPVNRVPARRAGNA
zo02_225	61	NADELIGSAMGLNE	QPVLPVNRVPARRAGNA
zo04_225	61	NADELIGSAMGLNF	QPVLPVNRVPARRAGNA
zo06_225	61	NADELIGSAMGLNE	QPVLPVNRVPARRAGNA
zo07_225	61	NADELIGSAMGLNE	QPVLPVNRVPARRAGNA
zo10_225	61	NADELIGSAMGLNE	QPVLPVNRVPARRAGNA
zo14_225	61	NADELIGSAMGLNE	QPVLPVNRVPARRAGNA
zo16_225	61	NADELIGSAMGLNE	QPVLPVNRVPARRAGNA
zo17_225	61	NADELIGSAMGLNE	QPVLPVNRVPARRAGNA
zo18_225	61	NADELIGSAMGLNE	QPVLPVNRVPARRAGNA
zo19_225	61	NADELIGSAMGLNE	QPVLPVNRVPARRAGNA
zo21_225	61	NADELIGSAMGLNE	QPVLPVNRVPARRAGNA
zo27_225	61	NADELIGSAMGLNE	QPVLPVNRVPARRAGNA
zo28_225	61	NADELIGSAMGLNE	QPVLPVNRVPARRAGNA
zo29_225	61	NADELIGSAMGLNE	QPVLPVNRVPARRAGNA
zo13_225	61	NADELIGSAMGLNE	QPVLPVNRVPARRAGNA
zo03_225	61	NADELIGSAMGLNF	QPVLPVNRVPARRAGNA
zo15_225	61	NADELIGSAMGLNE	QPVLPVNRVPARRAGNA
fa1090	61	NADELIGSAMGLNE	QPVLPVNRVPARRAGNA
zo32_225	61	NADELIGSAMGLNE	QPVLPVNRVPARRAGNA
zo33_225	61	NADELIGSAMGLNE	QPVLPVNRVPARRAGNA

Fig. 19A

Fig. 19B

zo05_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo08_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
z2491	241	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo11_225	241	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo20_225	241	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo01_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo09_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo12_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo22_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo23_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo24_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo25_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo26_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo96_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo02_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo04_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo06_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo07_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo10_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo14_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo16_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo17_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo18_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo19_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo21_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo27_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo28_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo29_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo13_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo03_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo15_225	183	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
fa1090	183	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo32_225	183	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo33_225	183	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*

Fig. 19C

Fig. 20A

gnmzq09	121	YQILDSDTTVSAKARLVDLSRNGKVLWSGSASIREGSNNNSGLLGALV	SAVNQIANSLT
gnmzq31	121	YQILDSDTTVSAKARLVDLSRNGKVLWSGSASIREGSNNNSGLLGALV	SAVNQIANSLT
fa1090	121	YQILDSDTTVSAKARLVDLSRNGKELWSGSASIREGSNNNSGLLGALV	SAVNQIANSLT
gnmzq32	121	YQILDSDTTVSAKARLVDLSRNGKELWSGSASIREGSNNNSGLLGALV	SAVNQIANSLT
gnmzq33	121	YQILDSDTTVSAKARLVDLSRNGKELWSGSASIREGSNNNSGLLGALV	SAVNQIANSLT
gnmzq01	121	YQILDSDTTVSAKARLVDLSRNGKELWSGSASIREGSNNNSGLLGALV	SAVNQIANSLT
gnmzq05	121	YQILDSDTTVSAKARLVDLSRNGKELWSGSASIREGSNNNSGLLGALV	SAVNQIANNLT
gnmzq08	121	YQILDSDTTVSAKARLVDLSRNGKELWSGSASIREGSNNNSGLLGALV	SAVNQIANNLT
gnmzq02	121	YQILDSDTTVSAKARLVDLSRNGKELWSGSASIREGSNNNSGLLGALV	SAVNQIANNLT
gnmzq03	121	YQILDSDTTVSAKARLVDLSRNGKELWSGSASIREGSNNNSGLLGALV	SAVNQIANNLT
gnmzq04	121	YQILDSDTTVSAKARLVDLSRNGKELWSGSASIREGSNNNSGLLGALV	SAVNQIANSLT
gnmzq07	121	YQILDSDTTVSAKARLVDLSRNGKELWSGSASIREGSNNNSGLLGALV	SAVNQIANSLT
gnmzq10	121	YQILDSDTTVSAKARLVDLSRNGKELWSGSASIREGSNNNSGLLGALV	SAVNQIANSLT
gnmzq11	121	YQILDSDTTVSAKARLVDLSRNGKELWSGSASIREGSNNNSGLLGALV	SAVNQIANSLT
gnmzq13	121	YQILDSDTTVSAKARLVDLSRNGKELWSGSASIREGSNNNSGLLGALV	SAVNQIANSLT
gnmzq15	121	YQILDSDTTVSAKARLVDLSRNGKELWSGSASIREGSNNNSGLLGALV	SAVNQIANSLT
gnmzq16	121	YQILDSDTTVSAKARLVDLSRNGKELWSGSASIREGSNNNSGLLGALV	SAVNQIANSLT
gnmzq17	121	YQILDSDTTVSAKARLVDLSRNGKELWSGSASIREGSNNNSGLLGALV	SAVNQIANSLT
gnmzq19	121	YQILDSDTTVSAKARLVDLSRNGKELWSGSASIREGSNNNSGLLGALV	SAVNQIANSLT
gnmzq21	121	YQILDSDTTVSAKARLVDLSRNGKELWSGSASIREGSNNNSGLLGALV	SAVNQIANSLT
gnmzq22	121	YQILDSDTTVSAKARLVDLSRNGKELWSGSASIREGSNNNSGLLGALV	SAVNQIANSLT
gnmzq23	121	YQILDSDTTVSAKARLVDLSRNGKELWSGSASIREGSNNNSGLLGALV	SAVNQIANSLT
gnmzq24	121	YQILDSDTTVSAKARLVDLSRNGKELWSGSASIREGSNNNSGLLGALV	SAVNQIANSLT
gnmzq25	121	YQILDSDTTVSAKARLVDLSRNGKELWSGSASIREGSNNNSGLLGALV	SAVNQIANSLT
gnmzq27	121	YQILDSDTTVSAKARLVDLSRNGKELWSGSASIREGSNNNSGLLGALV	SAVNQIANSLT
gnmzq28	121	YQILDSDTTVSAKARLVDLSRNGKELWSGSASIREGSNNNSGLLGALV	SAVNQIANSLT
gnmzq29	121	YQILDSDTTVSAKARLVDLSRNGKELWSGSASIREGSNNNSGLLGALV	SAVNQIANSLT
z2491	121	YQILDSDTTVSAKARLVDLSRNGKELWSGSASIREGSNNNSGLLGALV	SAVNQIANSLT
gnmzq14	121	YQILDSDTTVSAKARLVDLSRNGKELWSGSASIREGSNNNSGLLGALV	SAVNQIANSLT
gnmzq18	121	YQILDSDTTVSAKARLVDLSRNGKELWSGSASIREGSNNNSGLLGALV	SAVNQIANSLT
gnmzq26	121	YQILDSDTTVSAKARLVDLSRNGKELWSGSASIREGSNNNSGLLGALV	SAVNQIANSLT
gnmzq09	181	DRGYQVS KTAAYNLLSPYSHNGILKGPRF VEEQPK*	
gnmzq31	181	DRGYQVS KTAAYNLLSPYSHNGILKGPRF VEEQPK*	
fa1090	181	DRGYQVS KTAAYNLLSPYSHNGILKGPRF VEEQPK*	
gnmzq32	181	DRGYQVS KTAAYNLLSPYSHNGILKGPRF VEEQPK*	
gnmzq33	181	DRGYQVS KTAAYNLLSPYSHNGILKGPRF VEEQPK*	
gnmzq01	181	DRGYQVS KTAAYNLLSPYSHNGILKGPRF VEEQPK*	
gnmzq05	181	DRGYQVS KTAAYNLLSPYSHNGILKGPRF VEEQPK*	
gnmzq08	181	DRGYQVS KTAAYNLLSPYSHNGILKGPRF VEEQPK*	
gnmzq02	181	DRGYQVS KTAAYNLLSPYSHNGILKGPRF VEEQPK*	
gnmzq03	181	DRGYQVS KTAAYNLLSPYSHNGILKGPRF VEEQPK*	
gnmzq04	181	DRGYQVS KTAAYNLLSPYSHNGILKGPRF VEEQPK*	
gnmzq07	181	DRGYQVS KTAAYNLLSPYSHNGILKGPRF VEEQPK*	
gnmzq10	181	DRGYQVS KTAAYNLLSPYSHNGILKGPRF VEEQPK*	
gnmzq11	181	DRGYQVS KTAAYNLLSPYSHNGILKGPRF VEEQPK*	
gnmzq13	181	DRGYQVS KTAAYNLLSPYSHNGILKGPRF VEEQPK*	
gnmzq15	181	DRGYQVS KTAAYNLLSPYSHNGILKGPRF VEEQPK*	
gnmzq16	181	DRGYQVS KTAAYNLLSPYSHNGILKGPRF VEEQPK*	
gnmzq17	181	DRGYQVS KTAAYNLLSPYSHNGILKGPRF VEEQPK*	
gnmzq19	181	DRGYQVS KTAAYNLLSPYSHNGILKGPRF VEEQPK*	
gnmzq21	181	DRGYQVS KTAAYNLLSPYSHNGILKGPRF VEEQPK*	
gnmzq22	181	DRGYQVS KTAAYNLLSPYSHNGILKGPRF VEEQPK*	
gnmzq23	181	DRGYQVS KTAAYNLLSPYSHNGILKGPRF VEEQPK*	
gnmzq24	181	DRGYQVS KTAAYNLLSPYSHNGILKGPRF VEEQPK*	
gnmzq25	181	DRGYQVS KTAAYNLLSPYSHNGILKGPRF VEEQPK*	
gnmzq27	181	DRGYQVS KTAAYNLLSPYSHNGILKGPRF VEEQPK*	
gnmzq28	181	DRGYQVS KTAAYNLLSPYSHNGILKGPRF VEEQPK*	
gnmzq29	181	DRGYQVS KTAAYNLLSPYSHNGILKGPRF VEEQPK*	
z2491	181	DRGYQVS KTAAYNLLSPYSHNGILKGPRF VEEQPK*	
gnmzq14	181	DRGYQVS KTAAYNLLSPYSHNGILKGPRF VEEQPK*	
gnmzq18	181	DRGYQVS KTAAYNLLSPYSHNGILKGPRF VEEQPK*	
gnmzq26	181	DRGYQVS KTAAYNLLSPYSHNGILKGPRF VEEQPK*	

Fig. 20B

287_14	1	MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSKPAAPVVSE	KETEA
287_2	1	MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSKPAAPVVSE	KETEA
287_21	1	MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSKPAAPVVSE	KETEA
z2491	1	MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSKPAAPVVSE	KETEA
287_9	1	MFKRSVIAMACIVALSACGGGGGGSPDVKSADTLSKPAAPVVSE	KETEA
fa1090	1	MFKRSVIAMACIFALSACGGGGGGSPDVKSADTPSKPAAPVVAENAGEGVLPKEKKDEEA	KETEA

287_14	50	KEDAPQAGSQGQGAPSXQGGQDMAAVSEENTGNNGGAATTDKPKNEDEGAQNDMPQNAADT
287_2	50	KEDAPQAGSQGQGAPSXQGGQDMAAVSEENTGNNGGAATTDKPKNEDEGAQNDMPQNAADT
287_21	50	KEDAPQAGSQGQGAPSXQGSQDMAAVSEENTGNNGGAATTDKPKNEDEGAQNDMPQNAADT
z2491	50	KEDAPQAGSQGQGAPSXQGSQDMAAVSEENTGNNGGAATVTADNPKNEDEVQAQNDMPQNAAGT
287_9	61	VSGAPQADT..QDATABKGQDMAAVSAENTGNNGGAATTADNPKNEDEVQAQNDMPQNAAGT
fal090	61	AGGAPQADT..QDATABAGEGSQDMAAVSAENTGNNGGAATTADNPKNEDAGAQNDMPQNAADT

287_14 110 D~~S~~T~~P~~NHTP~~A~~S~~N~~M~~P~~A~~G~~N~~M~~E~~N~~Q~~A~~P~~D~~A~~G~~E~~S~~E~~Q~~P~~A~~N~~Q~~P~~D~~M~~A~~N~~T~~A~~D~~G~~M~~Q~~G~~D~~D~~P~~S~~A~~G~~G~~E~~N~~A~~G~~N~~T~~A~~
287_2 110 D~~S~~T~~P~~NHTP~~A~~S~~N~~M~~P~~A~~G~~N~~M~~E~~N~~Q~~A~~P~~D~~A~~G~~E~~S~~E~~Q~~P~~A~~N~~Q~~P~~D~~M~~A~~N~~T~~A~~D~~G~~M~~Q~~G~~D~~D~~P~~S~~A~~G~~G~~E~~N~~A~~G~~N~~T~~A~~
287_21 110 D~~S~~~~S~~T~~P~~NHTP~~D~~P~~N~~M~~L~~A~~G~~N~~M~~E~~N~~Q~~A~~T~~D~~A~~G~~E~~S~~S~~Q~~P~~A~~N~~Q~~P~~D~~M~~A~~N~~T~~A~~D~~G~~M~~Q~~G~~D~~D~~P~~S~~A~~G~~G~~E~~N~~A~~G~~N~~T~~A~~
z2491 110 D~~S~~~~S~~T~~P~~NHTP~~D~~P~~N~~M~~L~~A~~G~~N~~M~~E~~N~~Q~~A~~T~~D~~A~~G~~E~~S~~S~~Q~~P~~A~~N~~Q~~P~~D~~M~~A~~N~~T~~A~~D~~G~~M~~Q~~G~~D~~D~~P~~S~~A~~G~~G~~E~~N~~A~~G~~N~~T~~A~~
287_9 119 D~~S~~~~S~~T~~P~~NHTP~~A~~P~~N~~M~~P~~~~T~~R~~D~~M~~G~~N~~O~~A~~P~~D~~A~~~~G~~E~~S~~S~~Q~~P~~A~~N~~Q~~P~~D~~M~~A~~N~~T~~A~~D~~G~~M~~Q~~G~~D~~D~~P~~S~~A~~G~~G~~E~~N~~A~~G~~N~~T~~A~~
fal090 117

287_14	170	AQ S TNOA E NNQ T AGS Q N P ASS T NP S AT N S G DF F G T N V I N S V I D G P S Q N I T L T H C K G D S
287_2	170	AQ S TNQ A E N NQ T AGS Q N P AS S TNP S AT N S G DF F G R T N V I N S V I D G P S Q N I T L T H C K G D S
287_21	170	AQ S ANQ A G N Q A AG S SD P IP A EN P AP A NG G S N F G R V D L I N G V I D G P S Q N I T L T H C K G D S
z2491	170	AQ S ANQ A G N Q A AG S SD P IP A EN P AP A NG G S N F G R V D L I N G V I D G P S Q N I T L T H C K G D S
287_9	178	DQ S ANQ A E N NQ V E G S Q N P ASS T NP N AT N GG S D F G R I N V G I K S G E N W T L H C K D R S
fal090	117	.ESANQ T GN N Q P AG S SD S AP A SN P AP A NG G S D E G R T N V I D G P S Q N I T L T H C K G D S

```

287_14 230 CSGNNFLDDEEVQIKSEFEKLSDAKISNYKKDGKNDGKNUKFVGLVADSQVMKGGINQYII
287_2 230 CSGNNFLDDEEVQIKSEFEKLSDAKISNYKKDGKNDGKNDKFVGLVADSQVMKGGINQYII
287_21 230 CSGNNFLDDEEVQIKSEFEKLSDAKISNYKKDGKNDGKNDKFVGLVADSQVMKGGINQYII
z2491 230 CSGNNFLDDEEVQIKSEFEKLSDAKISNYKK...DGKNDKVFVGLVADSQVMKGGINQYII
287_9 238 CDRD.FLDEEAPPKSEFEKLSDEKIKRYKK...DEQRNFVGLVADEWVKNGTNTKYII
fa1090 176 CNGDNFLDDEEAPS KSEFEKLSDEKIKRYKK...DEQRNFVGLVADRKVKDGTNKYII

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287_14 290 FYKPKKP. . . SFEARFRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSGNIFAPEG
287_2 290 FYKPKKP. . . SFEARFRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSGNIFAPEG
287_21 286 FYKPKKP. . . SFEARFRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSGNIFAPEG
z2491 286 FYKPKKP. . . SFEARFRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSGNIFAPEG
287_9 293 IYKDKSASSSSARFRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSGNIFAPEG
fal090 232 FYTDKPKP. . . RSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSGNIFAPEG

287_14	348	NYRYLTYGAEKLPGGSYALRVQGEPSKGEMLAGTAVYNGEVLHFHTENGRPSPLRGRFAA
287_2	348	NYRYLTYGAEKLPGGSYALRVQGEPSKGEMLAGTAVYNGEVLHFHTENGRPSPLRGRFAA
287_21	344	NYRYLTYGAEKLPGGSYALRVQGEPKGEMLAGTAVYNGEVLHFHTENGRPYPLRGRFAA
z2491	344	NYRYLTYGAEKLPGGSYALRVQGEPKGEMLAGTAVYNGEVLHFHTENGRPYPLRGRFAA
287_9	353	NYRYLTYGAEKLSGGSYALSVQGEPKGEMLAGTAVYNGEVLHFHTENGRPSPLRGRFAA
fa1090	285	NYRYLTYGAFKLPGGSYALRVQGEPKGEMLVGTAVYNGEVLHFHTENGRPYPLRGRFAA

287_14 408 KVDFGSKSVVDGI IDSGD GLHMGTQKFKAIDGNNGFKGTWTENG GGDVSGF FYGPAGEEVA
287_2 408 KVDFGSKSVVDGI IDSGD GLHMGTQKFKAIDGNNGFKGTWTENG GGDVSGF FYGPAGEEVA
287_21 404 KVDFGSKSVVDGI IDSGDD LHMGQTQKFKAIDGNNGFKGTWTENG SGDVSGF FYGPAGEEVA
z2491 404 KVDFGSKSVVDGI IDSGDD LHMGQTQKFKAIDGNNGFKGTWTENG SGDVSGF FYGPAGEEVA
287_9 413 KVDFGSKSVVDGI IDSGDD LHMGQTQKFKAIDGNNGFKGTWTENG SGDVSGF FYGPAGEEVA
fa1090 345 KVDFGSKSVVDGI IDSGDD LHMGQTQKFKAIDGNNGFKGTWTENG GGDVSGF FYGPAGEEVA

FIG. 21A

287_14	468	GKYSYRPTDAEKGGFGVFA <u>G</u> KKEQD*
287_2	468	GKYSYRPTDAEKGGFGVFA <u>G</u> KKEQD*
287_21	464	GKYSYRPTDAEKGGFGVFA <u>G</u> KKEQD*
z2491	464	GKYSYRPTDAEKGGFGVFA <u>G</u> KKEQD*
287_9	473	GKYSYRPTDAEKGGFGVFA <u>G</u> KKEQD*
fa1090	405	GKYSYRPTDAEKGGFGVFA <u>G</u> KKEQD*

FIG. 21B

z2491_519 1 MEFFIILLAAVVVFVGFKSFVVIPQQEVHVERLGRFHRLTAGLNILIPFIDRVAYRHSL
zv26_519 1 MEFFIILLAAVVVFVGFKSFVVIPQQEVHVERLGRFHRLTAGLNILIPFIDRVAYRHSL
zv22_519ass 1 MEFFIILLAAVVVFVGFKSFVVIPQQEVHVERLGRFHRLTAGLNILIPFIDRVAYRHSL
fa1090_519 1 MEFFIILLAAVVVFVGFKSFVVIPQQEVHVERLGRFHRLTAGLNILIPFIDRVAYRHSL
zv32_519 1 MEFFIILLAAVVVFVGFKSFVVIPQQEVHVERLGRFHRLTAGLNILIPFIDRVAYRHSL
zv11_519 1 MEFFIILLAAVVVFVGFKSFVVIPQQEVHVERLGRFHRLTAGLNILIPFIDRVAYRHSL
zv28_519 1 MEFFIILLAAVVVFVGFKSFVVIPQQEVHVERLGRFHRLTAGLNILIPFIDRVAYRHSL
zv96_519 1 MEFFIILLAAVVVFVGFKSFVVIPQQEVHVERLGRFHRLTAGLNILIPFIDRVAYRHSL
zv02_519 1 MEFFIILLAAVVVFVGFKSFVVIPQQEVHVERLGRFHRLTAGLNILIPFIDRVAYRHSL
zv03_519 1 MEFFIILLAAVVVFVGFKSFVVIPQQEVHVERLGRFHRLTAGLNILIPFIDRVAYRHSL
zv04_519 1 MEFFIILLAAVVVFVGFKSFVVIPQQEVHVERLGRFHRLTAGLNILIPFIDRVAYRHSL
zv05_519 1 MEFFIILLAAVVVFVGFKSFVVIPQQEVHVERLGRFHRLTAGLNILIPFIDRVAYRHSL
zv01_519 1 MEFFIILLAAVVVFVGFKSFVVIPQQEVHVERLGRFHRLTAGLNILIPFIDRVAYRHSL
zv07_519 1 MEFFIILLAAVVVFVGFKSFVVIPQQEVHVERLGRFHRLTAGLNILIPFIDRVAYRHSL
zv12_519 1 MEFFIILLAAVVVFVGFKSFVVIPQQEVHVERLGRFHRLTAGLNILIPFIDRVAYRHSL
zv18_519 1 MEFFIILLAAVVVFVGFKSFVVIPQQEVHVERLGRFHRLTAGLNILIPFIDRVAYRHSL
zv19_519 1 MEFFIILLAAVVVFVGFKSFVVIPQQEVHVERLGRFHRLTAGLNILIPFIDRVAYRHSL
zv21_519ass 1 MEFFIILLAAVVVFVGFKSFVVIPQQEVHVERLGRFHRLTAGLNILIPFIDRVAYRHSL
zv27_519 1 MEFFIILLAAVVVFVGFKSFVVIPQQEVHVERLGRFHRLTAGLNILIPFIDRVAYRHSL
zv20_519ass 1 MEFFIILLAAVVVFVGFKSFVVIPQQEVHVERLGRFHRLTAGLNILIPFIDRVAYRHSL
zv06_519ass 1 MEFFIILLAAVVVFVGFKSFVVIPQQEVHVERLGRFHRLTAGLNILIPFIDRVAYRHSL
zv29_519ass 1 MEFFIILLAAVVVFVGFKSFVVIPQQEVHVERLGRFHRLTAGLNILIPFIDRVAYRHSL

z2491_519 61 KEIPLDVPSQVCITRDNTQLTVGDIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv26_519 61 KEIPLDVPSQVCITRDNTQLTVGDIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv22_519ass 61 KEIPLDVPSQVCITRDNTQLTVGDIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
fa1090_519 61 KEIPLDVPSQVCITRDNTQLTVGDIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv32_519 61 KEIPLDVPSQVCITRDNTQLTVGDIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv11_519 61 KEIPLDVPSQVCITRDNTQLTVGDIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv28_519 61 KEIPLDVPSQVCITRDNTQLTVGDIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv96_519 61 KEIPLDVPSQVCITRDNTQLTVGDIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv02_519 61 KEIPLDVPSQVCITRDNTQLTVGDIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv03_519 61 KEIPLDVPSQVCITRDNTQLTVGDIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv04_519 61 KEIPLDVPSQVCITRDNTQLTVGDIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv05_519 61 KEIPLDVPSQVCITRDNTQLTVGDIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv01_519 61 KEIPLDVPSQVCITRDNTQLTVGDIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv07_519 61 KEIPLDVPSQVCITRDNTQLTVGDIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv12_519 61 KEIPLDVPSQVCITRDNTQLTVGDIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv18_519 61 KEIPLDVPSQVCITRDNTQLTVGDIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv19_519 61 KEIPLDVPSQVCITRDNTQLTVGDIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv21_519ass 61 KEIPLDVPSQVCITRDNTQLTVGDIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv27_519 61 KEIPLDVPSQVCITRDNTQLTVGDIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv20_519ass 61 KEIPLDVPSQVCITRDNTQLTVGDIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv06_519ass 61 KEIPLDVPSQVCITRDNTQLTVGDIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
zv29_519ass 61 KEIPLDVPSQVCITRDNTQLTVGDIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG

z2491_519 121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv26_519 121 RMELDKTFEERDEINSTVVALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv22_519ass 121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
fa1090_519 121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv32_519 121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv11_519 121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv28_519 121 RMELDKTFEERDEINSTVVALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv96_519 121 RMELDKTFEERDEINSTVVALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv02_519 121 RMELDKTFEERDEINSTVVALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv03_519 121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv04_519 121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv05_519 121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv01_519 121 RMELDKTFEERDEINSTVVALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv07_519 121 RMELDKTFEERDEINSTVVALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv12_519 121 RMELDKTFEERDEINSTVVALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv18_519 121 RMELDKTFEERDEINSTVVALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv19_519 121 RMELDKTFEERDEINSTVVALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv21_519ass 121 RMELDKTFEERDEINSTVVALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv27_519 121 RMELDKTFEERDEINSTVVALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv20_519ass 121 RMELDKTFEERDEINSTVVALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv06_519ass 121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv29_519ass 121 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE

FIG. 22A

z2491_519	181	KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv26_519	181	KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv22_519ass	181	KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
fa1090_519	181	KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv32_519	181	KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv11_519	181	KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv28_519	181	KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv96_519	181	KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv02_519	181	KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv03_519	181	KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv04_519	181	KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv05_519	181	KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv01_519	181	KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv07_519	181	KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv12_519	181	KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv18_519	181	KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv19_519	181	KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv21_519ass	181	KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv27_519	181	KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv20_519ass	181	KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv06_519ass	181	KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv29_519ass	181	KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR

z2491_519	241	LVAEANAEAIRQIAAAALQTQGGADAVNLKIAEQYVAFFNNLAKESNTLIMPANVADIGSL
zv26_519	241	LVAEANAEAIRQIAAAALQTQGGADAVNLKIAEQYVAFFNNLAKESNTLIMPANVADIGSL
zv22_519ass	241	LVAEANAEAIRQIAAAALQTQGGADAVNLKIAEQYVAFFNNLAKESNTLIMPANVADIGSL
fa1090_519	241	LVAEANAEAIRQIAAAALQTQGGADAVNLKIAEQYVAFFNNLAKESNTLIMPANVADIGSL
zv32_519	241	LVAEANAEAIRQIAAAALQTQGGADAVNLKIAEQYVAFFNNLAKESNTLIMPANVADIGSL
zv11_519	241	LVAEANAEAIRQIAAAALQTQGGADAVNLKIAEQYVAFFNNLAKESNTLIMPANVADIGSL
zv28_519	241	LVAEANAEAIRQIAAAALQTQGGADAVNLKIAEQYVAFFNNLAKESNTLIMPANVADIGSL
zv96_519	241	LVAEANAEAIRQIAAAALQTQGGADAVNLKIAEQYVAFFNNLAKESNTLIMPANVADIGSL
zv02_519	241	LVAEANAEAIRQIAAAALQTQGGADAVNLKIAEQYVAFFNNLAKESNTLIMPANVADIGSL
zv03_519	241	LVAEANAEAIRQIAAAALQTQGGADAVNLKIAEQYVAFFNNLAKESNTLIMPANVADIGSL
zv04_519	241	LVAEANAEAIRQIAAAALQTQGGADAVNLKIAEQYVAFFNNLAKESNTLIMPANVADIGSL
zv05_519	241	LVAEANAEAIRQIAAAALQTQGGADAVNLKIAEQYVAFFNNLAKESNTLIMPANVADIGSL
zv01_519	241	LVAEANAEAIRQIAAAALQTQGGADAVNLKIAEQYVAFFNNLAKESNTLIMPANVADIGSL
zv07_519	241	LVAEANAEAIRQIAAAALQTQGGADAVNLKIAEQYVAFFNNLAKESNTLIMPANVADIGSL
zv12_519	241	LVAEANAEAIRQIAAAALQTQGGADAVNLKIAEQYVAFFNNLAKESNTLIMPANVADIGSL
zv18_519	241	LVAEANAEAIRQIAAAALQTQGGADAVNLKIAEQYVAFFNNLAKESNTLIMPANVADIGSL
zv19_519	241	LVAEANAEAIRQIAAAALQTQGGADAVNLKIAEQYVAFFNNLAKESNTLIMPANVADIGSL
zv21_519ass	241	LVAEANAEAIRQIAAAALQTQGGADAVNLKIAEQYVAFFNNLAKESNTLIMPANVADIGSL
zv27_519	241	LVAEANAEAIRQIAAAALQTQGGADAVNLKIAEQYVAFFNNLAKESNTLIMPANVADIGSL
zv20_519ass	241	LVAEANAEAIRQIAAAALQTQGGADAVNLKIAEQYVAFFNNLAKESNTLIMPANVADIGSL
zv06_519ass	241	LVAEANAEAIRQIAAAALQTQGGADAVNLKIAEQYVAFFNNLAKESNTLIMPANVADIGSL
zv29_519ass	241	LVAEANAEAIRQIAAAALQTQGGADAVNLKIAEQYVAFFNNLAKESNTLIMPANVADIGSL

z2491_519	301	ISAGMKIIDSSKTAK*
zv26_519	301	ISAGMKIIDSSKTAK*
zv22_519ass	301	ISAGMKIIDSSKTAK*
fa1090_519	301	ISAGMKIIDSSKTAK*
zv32_519	301	ISAGMKIIDSSKTAK*
zv11_519	301	ISAGMKIIDSSKTAK*
zv28_519	301	ISAGMKIIDSSKTAK*
zv96_519	301	ISAGMKIIDSSKTAK*
zv02_519	301	ISAGMKIIDSSKTAK*
zv03_519	301	ISAGMKIIDSSKTAK*
zv04_519	301	ISAGMKIIDSSKTAK*
zv05_519	301	ISAGMKIIDSSKTAK*
zv01_519	301	ISAGMKIIDSSKTAK*
zv07_519	301	ISAGMKIIDSSKTAK*
zv12_519	301	ISAGMKIIDSSKTAK*
zv18_519	301	ISAGMKIIDSSKTAK*
zv19_519	301	ISAGMKIIDSSKTAK*
zv21_519ass	301	ISAGMKIIDSSKTAK*
zv27_519	301	ISAGMKIIDSSKTAK*
zv20_519ass	301	ISAGMKIIDSSKTAK*
zv06_519ass	301	ISAGMKIIDSSKTAK*
zv29_519ass	301	ISAGMKIIDSSKTAK*

Fig. 22B

Fig. 23A

Fig. 23B

Fig. 23C

fa1090	361	IDRH YITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm33asbc	361	IDRH YITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm32asbc	361	IDRH YITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm23asbc	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm27bc	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGE TAGK
zm09	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGE TAGK
zm10	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm24	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm25	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm14	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm04	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm11asbc	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm08n	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm96	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm01	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm02	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm03	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm07	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm12	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm18	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm19	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm20	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm21	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm06	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm17	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm13	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm05	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
z2491	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm22	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm26	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm28	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm29asbc	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm16	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm15	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm31asbc	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
fa1090	421	QKTTGYYWQLLPNGMKPEYRP*
zm33asbc	421	QKTTGYYWQLLPNGMKPEYRP*
zm32asbc	421	QKTTGYYWQLLPNGMKPEYRP*
zm23asbc	421	MKEF GYYWQLLPNGMKPEYRP*
zm27bc	421	MKEF GYYWQLLPNGMKPEYRP*
zm09	421	QKTTGYYWQLLPNGMKPEYRP*
zm10	421	QKTTGYYWQLLPNGMKPEYRP*
zm24	421	QKTTGYYWQLLPNGMKPEYRP*
zm25	421	QKTTGYYWQLLPNGMKPEYRP*
zm14	421	QKTTGYYWQLLPNGMKPEYRP*
zm04	421	QKTTGYYWQLLPNGMKPEYRP*
zm11asbc	421	QKTTGYYWQLLPNGMKPEYRP*
zm08n	421	QKTTGYYWQLLPNGMKPEYRP*
zm96	421	QKTTGYYWQLLPNGMKPEYRP*
zm01	421	QKTTGYYWQLLPNGMKPEYRP*
zm02	421	QKTTGYYWQLLPNGMKPEYRP*
zm03	421	QKTTGYYWQLLPNGMKPEYRP*
zm07	421	QKTTGYYWQOLLPGNMKPEYRP*
zm12	421	QKTTGYYWQOLLPGNMKPEYRP*
zm18	421	QKTTGYYWQOLLPGNMKPEYRP*
zm19	421	QKTTGYYWQOLLPGNMKPEYRP*
zm20	421	QKTTGYYWQOLLPGNMKPEYRP*
zm21	421	QKTTGYYWQOLLPGNMKPEYRP*
zm06	421	QKTTGYYWQOLLPGNMKPEYRP*
zm17	421	QKTTGYYWQOLLPGNMKPEYRP*
zm13	421	QKTTGYYWQOLLPGNMKPEYRP*
zm05	421	QKTTGYYWQOLLPGNMKPEYRP*
z2491	421	QKTTGYYWQOLLPGNMKPEYRP*
zm22	421	QKTTGYYWQOLLPGNMKPEYRP*
zm26	421	QKTTGYYWQOLLPGNMKPEYRP*
zm28	421	QKTTGYYWQOLLPGNMKPEYRP*
zm29asbc	421	QKTTGYYWQOLLPGNMKPEYRP*
zm16	421	QKTTGYYWQOLLPGNMKPEYRP*
zm15	421	QKTTGYYWQOLLPGNMKPEYRP*
zm31asbc	421	QKTTGYYWQOLLPGNMKPEYRP*

Fig. 23D





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(21) International Application Number:	PCT/US99/09346	(US). MASIGNANI, Vega [IT/IT]; Chiron S.p.A., Via Fiorentina, 1, I-53100 Siena (IT). MORA, Marirosa [IT/IT]; Chiron S.p.A., Via Fiorentina, 1, I-53100 Siena (IT). PETERSEN, Jeremy [US/US]; Arlington, VA (US). PIZZA, Mariagratis [IT/IT]; Chiron S.p.A., Via Fiorentina, 1, I-53100 Siena (IT). RAPPUOLI, Rino [IT/IT]; Chiron S.p.A., Via Fiorentina, 1, I-53100 Siena (IT). RATTI, Giulio [IT/IT]; Chiron S.p.A., Via Fiorentina, 1, I-53100 Siena (IT). SCALATO, Enzo [IT/IT]; Chiron S.p.A., Via Fiorentina, 1, I-53100 Siena (IT). SCARSELLI, Maria [IT/IT]; Chiron S.p.A., Via Fiorentina, 1, I-53100 Siena (IT). TETTELIN, Herve [US/US]; Gaithersburg, MD (US). VENTER, J., Craig [US/US]; Rockville, MD (US).
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(72) Inventors; and		
(75) Inventors/Applicants (for US only): FRASER, Claire [US/US]; Rockville, MD (US). GALEOTTI, Cesira [IT/IT]; Chiron S.p.A., Via Fiorentina, 1, I-53100 Siena (IT). GRANDI, Guido [IT/IT]; Chiron S.p.A., Via Fiorentina, 1, I-53100 Siena (IT). HICKEY, Erin [US/US]; Gaithersburg, MD		(81) Designated States: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).
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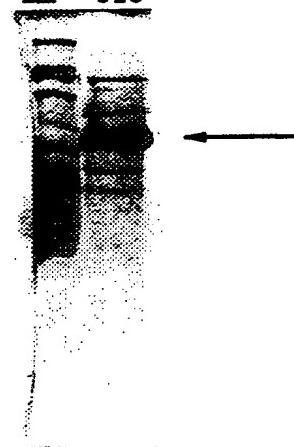
(57) Abstract

The invention provides proteins from *Neisseria meningitidis*, including the amino acid sequences and the corresponding nucleotide sequences. The proteins are predicted to be useful antigens for vaccines and/or diagnostics.

919 (46 kDa)

PURIFICATION

M1 919



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INTERNATIONAL SEARCH REPORT

International Application No
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A. CLASSIFICATION OF SUBJECT MATTER

IPC 6 C12N15/31 C07K14/22 C07K16/12 C12Q1/68 A61K39/095
G01N33/50

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 6 C12N C07K C12Q A61K G01N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>DATABASE TREMBL [Online] EMBL ID Q55666, AC Q55666, 1 November 1996 (1996-11-01) TABATA S: "Membrane-bound lytic transglycosylase A MltA Synechocystis sp. strain PCC 6803" XP002130156 Note: 100% aa seq identity of aa 342-350 with aa 392-400 of SEQ ID NOS 2790 and 2792, 27.6% (26.9%) aa seq identity with SEQ ID NO:2790 (2792) in 370 (387) aa overlap. the whole document</p> <p>---</p> <p>- / --</p>	1,4-6,9, 12

 Further documents are listed in the continuation of box C. Patent family members are listed in annex.

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van de Kamp, M

INTERNATIONAL SEARCH REPORT

International Application No

PL./US 99/09346

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	EP 0 818 465 A (BIOLOG MOLECULAIRE DES PLANTES ; INST OF MOLECULAR BIOTECHNOLOG (DE) 14 January 1998 (1998-01-14) Note: 100% nt seq identity of nt 367951-367961 of SEQ ID NO:1 with nt 163-173 of SEQ ID NO:2789. page 108 ---	8,11,12
A	LOMMATZSCH J ET AL.: "Outer membrane localization of murein hydrolases: MltA, a third lipoprotein lytic transglycosylase in Escherichia coli" JOURNAL OF BACTERIOLOGY, vol. 179, no. 17, September 1997 (1997-09), pages 5465-5470, XP002130154 Note: 33.7% (35.7%) aa seq identity with SEQ ID NO:2790 (2792) in 273 (207) aa overlap. abstract ---	1-12
A	DILLARD J P ET AL.: "A peptidoglycan hydrolase similar to bacteriophage endolysins acts as an autolysin in Neisseria gonorrhoeae" MOLECULAR MICROBIOLOGY, vol. 25, no. 5, September 1997 (1997-09), pages 893-901, XP000878964 abstract ---	1-12
A	WO 96 29412 A (IAF BIO VAC INC ; BRODEUR BERNARD R (CA); MARTIN DENIS (CA); HAMEL) 26 September 1996 (1996-09-26) cited in the application the whole document examples 1-12 ---	1-18
A	WO 94 08013 A (OREGON STATE) 14 April 1994 (1994-04-14) the whole document examples 1-7 ---	1-18
A	WO 92 13871 A (UNIV WASHINGTON) 20 August 1992 (1992-08-20) the whole document examples 1-10 ---	1-18
A	BLAKE M S ET AL.: "Vaccines for gonorrhoea: where are we on the curve?" TRENDS IN MICROBIOLOGY, vol. 3, no. 12, December 1995 (1995-12), pages 469-474, XP000876514 the whole document ---	1-18
	-/-	

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 99/09346

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Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	POOLMAN J T: "Development of a meningococcal vaccine" INFECTIOUS AGENTS AND DISEASE, vol. 4, no. 1, March 1995 (1995-03), pages 13-28, XP000876540 the whole document ---	1-18
X	WO 96 01901 A (RHONE POULENC RORER SA ;BLANC VERONIQUE (FR); THIBAUT DENIS (FR);) 25 January 1996 (1996-01-25) Note: 100% nt seq ident of bp 170-156 of SEQ ID NO:1 (rev DNA) with bp 202-216 of SEQ ID NO:1 (61.2% in 348 bp overlap), 40.7% seq ident of transl SEQ ID NO:1 with SEQ ID NO:2 in 118 aa overlap. page 102-104 example 1 ---	8,11,12
X	WO 97 37044 A (ASTRA AB ;ALM RICHARD A (US); SMITH DOUGLAS (US)) 9 October 1997 (1997-10-09) Note: 100% aa seq identity of aa 204-211, 186-193 & 352-359 of transl SEQ ID NOs 227, 345 & 1003, resp., with aa 59-66 of SEQ ID NO:2, 37.4% aa seq identity with SEQ ID NO:2 in 115 aa overlap. page 268-269 page 344 page 909-910 page 23, paragraph B.4 ---	4,12-14
X	DATABASE SWISSPROT [Online] ID YPCP_YEREN, AC P31485, 1 July 1993 (1993-07-01) BAEUMLER A J ET AL.: "Hypothetical 29.6 kD protein in PCP 5' region (ORF1)" XP002138650 Note: 100% aa seq identity of aa 148-159 with aa 140-151 of SEQ ID NO:442, 43.4% aa seq identity with SEQ ID NO:442 in 256 aa overlap. the whole document -& BAUMLER A J ET AL.: "A lipoprotein of Yersinia enterocolitica facilitates ferrioxamine uptake in Escherichia coli" JOURNAL OF BACTERIOLOGY, vol. 174, no. 3, February 1992 (1992-02), pages 1029-1035, XP000907295 page 1031, left-hand column, line 11 -right-hand column, line 15 ---	4,12
A	-/-	4,12

INTERNATIONAL SEARCH REPORT

International Application No

PL /US 99/09346

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>DATABASE SWISSPROT [Online] ID YDHH_HAEIN, AC P44861, 1 November 1995 (1995-11-01) FLEISCHMANN R D ET AL.: "Hypothetical protein HI0753" XP002138651 Note: 100% aa seq identity of aa 143-156 with aa 140-153 of SEQ ID NO:442, 41.6% aa seq identity with SEQ ID NO:442 in 377 aa overlap. the whole document</p> <p>---</p>	4,12
X	<p>WO 96 33276 A (HUMAN GENOME SCIENCES INC ;UNIV JOHNS HOPKINS (US)) 24 October 1996 (1996-10-24) Note: 100% nt seq identity of bp 816794-816807 with bp 289-302 of SEQ ID NO:441 (54.3% in 484 bp overlap), 100% aa seq identity of translated sequence with SEQ ID NO:442 in 14 aa overlap. page 77.488 Note: 100% nt seq identity of bp 230516-230526 with bp 1501-1511 of SEQ ID NO:489 (57.4% in 1292 bp overlap), 100% aa seq identity of translated sequence with SEQ ID NO:490 in 13 aa overlap. page 77.139 page 76.37, line HI0215 Note: 100% nt seq identity of bp 1025409-1025418 with bp 1339-1330 (rev strand) of SEQ ID NO:1201 (72.0% in 50 bp overlap). page 77.612</p> <p>---</p>	4,8, 11-14
X	<p>CONLIN C A ET AL.: "Escherichia coli prlC encodes an endopeptidase and is homologous to the Salmonella typhimurium opdA gene" JOURNAL OF BACTERIOLOGY, vol. 174, no. 18, September 1992 (1992-09), pages 5881-5997, XP000907300 Note: 100% nt seq ident of bp 1824-1837 with bp 1480-1493 of SEQ ID NO:489 (59.7% in 1282 bp overlap), 100% aa seq ident of aa 495-507 with aa 492-504 of SEQ ID NO:490 (49.5% in 679 aa overlap). abstract figure 2</p> <p>---</p> <p>-/-</p>	4,8,11, 12

INTERNATIONAL SEARCH REPORT

International Application No
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C(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>DATABASE SWISSPROT [Online] ID OPDA_HAEIN, AC P44573, 1 November 1995 (1995-11-01) FLEISCHMANN R D ET AL.: "Oligopeptidase A (EC 3.4.24.70)" XP002138652 Note: 100% aa seq identity of aa 496-508 with aa 492-504 of SEQ ID NO:490, 49.0% aa seq identity in 677 aa overlap. the whole document</p> <p>---</p>	4,12
X	<p>ROKBI B ET AL.: "Evaluation of recombinant transferrin - binding protein B variants from <i>Neisseria meningitidis</i> for their ability to induce cross-reactive and bactericidal antibodies against a genetically diverse collection of serogroup B strains." <i>INFECTION AND IMMUNITY</i>, vol. 65, no. 1, January 1997 (1997-01), pages 55-63, XP002138643 abstract</p> <p>---</p>	5
P,A	<p>DATABASE TREMBL [Online] EMBL ID 069750, AC 069750, 1 August 1998 (1998-08-01) ROKBI B ET AL.: "Transferrin binding protein B, TbpB, <i>Neisseria meningitidis</i>" XP002138653 Note: 22.3% aa seq identity with SEQ ID NO:1202 in 488 aa overlap. the whole document</p> <p>-& ROKBI B ET AL.: "Heterogeneity of tpbB, the transferrin-binding protein B gene, among serogroup B <i>Neisseria</i> <i>meningitidis</i> strains of the ET-5 complex" <i>CLINICAL AND DIAGNOSTIC LABORATORY</i> <i>IMMUNOLOGY</i>, vol. 4, no. 5, September 1997 (1997-09), pages 522-529, XP002138644 abstract</p> <p>---</p>	4,8, 12-15,17
A	<p>---</p> <p>-/-</p>	5,8, 12-15,17

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 99/09346

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	<p>DATABASE GCG_GENESEQ [Online] ID W14640, AC W14640, 5 March 1998 (1998-03-05) QUENTIN-MILLET M J ET AL.: "N. meningitidis HTR Tbp2 (de13777-385, de1407-465, de1488-508)" XP002138654 Note: 23.5% aa seq identity with SEQ ID NO:1202 in 571 aa overlap. the whole document</p> <p>-& WO 97 13860 A (PASTEUR MERIEUX SERUMS VACC; QUENTIN MILLET MARIE JOSE (FR); ROKBI)) 17 April 1997 (1997-04-17) claim 11</p> <p>---</p>	4,8, 12-15,17
A		4,8, 12-15,17
X	<p>DATABASE EMPR01 [Online] EMBL ID AF034831, AC AF034831, 4 December 1997 (1997-12-04) YOU Z ET AL.: "Rhizobium etli stomatin like protein (slp) gene, complete cds." XP002138655 Note: 100% nt seq ident of bp 4384-4395 with bp 529-540 of SEQ ID NO:1455 (54.4% in 638 bp overlap), 100% aa seq ident of aa 1394-1403 with aa 109-118 of SEQ ID NO:1456 (41.2% in 182 aa overlap). the whole document</p> <p>-& YOU Z ET AL.: "A stomatin-like protein encoded by the slp gene of Rhizobium etli is required for nodulation competitiveness on the common bean" MICROBIOLOGY, vol. 144, no. 9, September 1998 (1998-09), pages 2619-2627, XP000907294 abstract figure 2</p> <p>---</p>	4,8,11, 12
P,X		4,8,11, 12
X	<p>HUANG M ET AL.: "A stomatin-like protein necessary for mechanosensation in C. elegans" NATURE, vol. 378, no. 6554, 16 November 1995 (1995-11-16), pages 292-295, XP002138646 Note: 100% aa seq identity of aa 233-239 with aa 110-117 of SEQ ID NO:1456, 29.9% aa seq identity in 234 aa overlap. abstract figure 1</p> <p>---</p> <p>-/-</p>	4,12

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C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>WONG C Y ET AL.: "Cloning and characterization of two immunophilin-like genes, ilpA and fkpA, on a single 3.9-kilobase fragment of <i>Aeromonas hydrophila</i> genomic DNA" <i>JOURNAL OF BACTERIOLOGY</i>, vol. 179, no. 11, June 1997 (1997-06), pages 3397-3403, XP002138647 Note: 100% nt seq ident of bp 2659-2672 with bp 613-626 of SEQ ID NO:1745 (59.2% in 655 bp overlap), 100% aa seq ident of aa 205-216 with aa 200-211 of SEQ ID NO:1746 (44.9% in 265 aa overlap). abstract figure 2 ---</p>	4,8, 11-14
X	<p>DATABASE EMPR02 [Online] EMBL ID NE01198, AC U001198, 23 November 1993 (1993-11-23) MCALLISTER C F ET AL.: "<i>Neisseria elongata</i> NRL FKBP immunophilin homolog gene" XP002138656 Note: 100% nt seq identity of bp 125-138 with bp 635-648 of SEQ ID NO:1745 (65.8% nt seq identity in 237 bp overlap). the whole document</p>	8,11,12
X	<p>-& MCALLISTER C F ET AL.: "Analysis in <i>Neisseria meningitidis</i> and other <i>Neisseria</i> species homologous to the FKBP immunophilin family" <i>MOLECULAR MICROBIOLOGY</i>, vol. 10, no. 1, October 1993 (1993-10), pages 13-23, XP000907304 abstract figure 3 ---</p>	8,11,12
X	<p>SAMPSON B A ET AL.: "<i>Neisseria meningitidis</i> encodes an FK506-inhibitable rotamase" PROC. NAT'L. ACAD. SCI. USA, vol. 89, no. 4, 15 February 1992 (1992-02-15), pages 1164-1168, XP002138648 Note: 100% nt seq identity of bp 278-288 (284-294) with bp 719-729 of SEQ ID NO:1745 (60.5% nt seq identity in 281 bp overlap). abstract figure 2 ----</p>	8,11,12
	-/-	

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 99/09346

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	HACKER J ET AL.: "Immunophilins: structure-function relationship and possible role in microbial pathogenicity." MOLECULAR MICROBIOLOGY, vol. 10, no. 3, November 1993 (1993-11), pages 445-456, XP000907321 abstract ---	13,14,17
X	DATABASE EMPR01 [Online] EMBL ID ECUW93, AC U14003 (partial), 30 November 1994 (1994-11-30) BURLAND V ET AL.: "Escherichia coli K-12 chromosomal region from 92.8 to 00.1 minutes" XP002138657 Note: 100% nt seq identity of bp 37827-37839 with bp 1186-1174 of SEQ ID NO:2791. page 4 -----	8,11,12

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US 99/09346

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. Claims Nos.: because they relate to subject matter not required to be searched by this Authority, namely:

2. Claims Nos.: because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:

3. Claims Nos.: because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.

2. As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
1,3,16,18 (all completely); 2,4-15,17 (all partially). Inventions searched:
#1 (SEQ ID NOS 2789/2790), #2 (1/2), #222 (441/442), #246 (489/490), #602 (1201/1202), #729 (1455/1456), #874 (1745/1746), #1397 (2791/2792)

4. No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- The additional search fees were accompanied by the applicant's protest.
- No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

Invention 1. Claims: 1,3,16,18 (all completely); 2,4-15,17 (all partially)

A protein comprising the amino sequence of SEQ ID NO:2790 or comprising a fragment of at least 7 (preferably consecutive) amino acids of said SEQ ID NO; a protein with 50% or greater homology to said protein(s); an antibody binding to said protein(s); a nucleic acid encoding said protein(s), preferably comprising the nucleotide sequence of SEQ ID NO:2789 or a fragment comprising 10 or more consecutive nucleotides thereof; complementary nucleic acid molecules; compositions comprising said protein(s), nucleic acid(s) or antibody for vaccination, diagnosis or pharmaceutical use, preferably immunogenic compositions comprising said protein(s), and the use of said composition(s).

Invention 2. Claims: 2,4-15,17 (all partially)

A protein comprising an amino sequence according to SEQ ID NO:2 or comprising a fragment of at least 7 consecutive amino acids of said SEQ ID NO; an antibody binding to said protein(s); a nucleic acid encoding said protein(s), preferably comprising a nucleotide sequence according to SEQ ID NO:1 or a fragment comprising 10 or more consecutive nucleotides thereof; complementary nucleic acid molecules; compositions comprising said protein(s), nucleic acid(s) or antibody for vaccination, diagnosis or pharmaceutical use, preferably immunogenic compositions comprising said protein(s), and the use of said composition(s).

Inventions 3-1510. Claims: 2,4,-15,17 (all partially)

Same as invention 2 but for proteins limited to the even-numbered SEQ ID NOs:4-3020 except 2790, and for nucleic acids limited to the corresponding odd-numbered SEQ ID NOs:3-3019 except 2789. E.g., invention 3: limited to SEQ ID NO:4 and SEQ ID NO:3, invention 4: limited to SEQ ID NO:6 and SEQ ID NO:5, . . . , invention 1509: limited to SEQ ID NO:3018 and SEQ ID NO:3017, and invention 1510: limited to SEQ ID NO:3020 and SEQ ID NO:3019.

INTERNATIONAL SEARCH REPORT

format patent family members

International Application No
PCT/US 99/09346

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